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X82941 A. radiobact
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ALIGNMENTS

## VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE RESULT 1 AX958629 LOCUS DEFINITION ACCESSION ORIGIN FEATURES Query Match Best Local Similarity Matches 458; Conserv JOURNAL source Sequence 2 from Patent WO03100063. AX958629 AX958629.1 GI:40879469 Her Majesty The Queen in Right of Canada, Minister of Agriculture and Agri-Food (CA) Location/Qualifiers Hannoufa,A., Hegedus,D. and Bate,N. A repressor-mediated regulation system synthetic construct synthetic construct expression in plants Patent: WO 03100063-A 2 04-DEC-2003; other sequences; artificial sequences. AX958629 100.0%; Score 458; DB 2; ilarity 100.0%; Pred. No. 1.2e-129; Conservative 0; Mismatches 0; /organism="synthetic construct" /mol type="unassigned DNA" /db\_xref="reaxon:32630" /note="synthetic ROS optimized for plant codon under synthetic ROS and nuclear localization 1. .458 458 bp DNA for as Length 458; Indels control of linear Represented; by The codon usage PAT 14-JAN-2004 0; gene Gaps 0

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GTTGCTGCTTACGTTTCTAACCACGTTGTTCCTGTTACTGAGCTTCCTGGACTTATCTCT

GATGTTCATACTGCACTTTCTGGAACATCTGCTCCTGCTTCTGTTGCTGTTAACGTTGAG GATGTTCATACTGCACTTTCTGGAACATCTGCTCCTGCTTCTGTTGCTGTTAACGTTGAG

180 180 120 120 60 60

1 ATGACTGAGACTGCTTACGGTAACGCTCAGGATCTTCTTGTTGAGCTTACTGCTGATATC

ATGACTGAGACTGCTTACGGTAACGCTCAGGATCTTCTTGTTGAGCTTACTGCTGATATC

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REFERENCE
AUTHORS
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KEYWORDS
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                                                         AAGCAGAAGCCTGCTGTTTCTGTTCGTAAGTCTGTTCAGGATGATCATATCGTTTTGTTTTG
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/mol_type="unassigned DNA"
/mb xref="traxon:32630"
/mb xref="traxon:32630"
/note="synthetic ROS optimized for concoding fusion of ROS and nuclear
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                                                              TACGCTGAGGCTCGTTCTCGCTTAAGGAGATGGGTCTCGGTCAGCGTCGTAAGGCT
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/db_xref="taxon:32630"
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Sequence 3 from Patent WO03104462.
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Hannoufa, A.,
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/mol_type="unassigned DNA"
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Lydiate, D.J.
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                                                                                            expression in plants
Patent: WO 02095021-A 3 28-NOV-2002;
The Minister of Agriculture and Agri-Food
Location/Qualifiers
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                                                                                                                                                                                        Hannoufa, A., Hegedus, D. and
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                                                                                                                                                                                                                              sequences; artificial sequences.
  /organism="synthetic construct"
/mol type="unassigned DNA"
/gbe="taxon:32630"
/noTe="ROS consensus sequence"
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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58.3%;
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Sequence 1 from Patent WO03100063.
AX958628
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Patent: WO 03100063-A 1 04-DEC-2003;
Her Majesty The Queen in Right of Canada,
Minister of Agriculture and Agri-Food (CA)
Location/Qualifiers
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Agrobacterium tumefaciens
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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                                                  ATGACTGAGACTGCTTACGGTAACGCTCAGGATCTTCTTGTTGAGCCTTACTGCTGATATC
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                                                                                                                                                       /organism="Agrobacterium tumefaciens"
/mol_type="unassigned DNA"
/db_xref="taxon:358"
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                                                                                                 63.7%;
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Pred. No. 2.2e-78;
0; Mismatches 84;
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Sequence 1 from Patent WO02095021.
AX685341 GI:29371664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agrobacterium tumefaciens (Rhizobium radiobacter)
Agrobacterium tumefaciens
Bacteria; Proteobacteria; Alphaproteobacteria; Rh
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                                                                                                                                                                                                                                                                                                                                                                                                               expression in plants Patent: WO 02095021-A 1 28-NOV-2002;
                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          A repressor-mediated regulation system
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hannoufa, A., Hegedus, D. and Bate,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhizobiaceae; Agrobacterium
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                                                                                                                                            GIGGCIGCCIATGITAGCAACCACGICGITCCGGIAACTGAGCITCCCGGCCITATTICG
                                                                                                                                                               GTTGCTGCTTACGTTTCTAACCACGTTGTTCCTGTTACTGAGCTTCCTGGACTTATCTCT 120
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GAGTGTGGTTGTTTCAAGTCTCTCAAGCGTCACCTTACTACTCATCACTCTATGACT
                                                                                    GATGTTCATACGGCACTCAGCGGAACATCGGCACCGGCATCGGTGGCGGTCAATGTTGAA 180
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                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                           /organism="Agrobacterium tumefaciens"
/mol_type="unassigned DNA"
/db_xref="taxon:358"
                                                                                                                                                                                                                                                                    63.7%;
                                                                                                                                                                                                                                                       Score 291.6; DB 2
Pred. No. 2.2e-78;
0; Mismatches 84
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29-MAR-2003

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PUBMED
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cooley,M.B., D'Souza,M.R. and Kado,C.I.
The virC and virD operons of the Agrobacterium Ti,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhizobiaceae; Agrobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agrobacterium tumefaciens
Agrobacterium tumefaciens
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                                           /codon_start=1
/transI table=11
/product="ros protein"
/protein_id="AAA22106.1"
/db_xref="GI:142275"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               426
                                                                                                                                                                                                                                                                                                                                                                         order(189. .197,202. .210)
/gene="ros"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source text: A.tumefaciens Location/Qualifiers
/translation="MTETAYGNAQDLLVELTADIVAAYVSNHVVPVTELPGLISDVHT
ALSGTSAPASVAVNVEKQKPAVSVRKSVQDDHIVCLECGGSFKSLKRHLTTHHSMTPE
EYREKWDLPVDYPMVAPAYAEARSRLAKEMGLGQRRKANR"
                                                                                                                                  /gene="ros"
/function="specifically represses the virC and virD
operons in the virulence region of the Ti plasmid"
/experiment="experimental evidence, no additional details
                                                                                                                                                                                                                                           /gene="ros"
/note="inverted
202. .210
                                                                                                                                                                                                                                                                                                                                                                   order (189
                                                                                                                     recorded"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="ros"
/note="putative; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Agrobacterium tumefaciens"
/mol_type="genomic DNA"
                                                                                                                                                                                                                          gene="ros"
                                                                                                                                                                                                                                                                                                                     /note="putative; putative"
function="autoregulation repressor binding site"
                                                                                                                                                                                                                                                                                                                                              standard_name="ros-binding box"
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                                                                                                                                                                                                             'note="inverted repeat'
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89. .197
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                                                                                                                                                                                                                                                                                                                           Agrobacterium tumefaciens str. C58 of 254 of the complete sequence.
AE008022 AE007869
AE008022.1 GI:151559nn
                                                                                            Submitted (14-AUG-2001) Cereon Cambridge, MA 02139, USA Location/Qualifiers
                                                                                                                                                                                                      1 (bases 1 to 10212)
Hinkle,G., Slater,S.C. and Goodner,B.
Complete Genome Sequence of Agrobacterium tumefaciens C58
(Rhizobium radiobacter C58), the Causative Agent of Crown
                                                                                                                                                                                                                                                                          Agrobacterium tumefaciens str. C58
Agrobacterium tumefaciens str. C58
Bacteria; Proteobacteria; Alphaproteobacteria;
                                                                                                                                     2 (bases 1 to 10212)
Hinkle,G., Slater,S.C.
Direct Submission
                                                                                                                                                                                                                                                              Rhizobiaceae; Agrobacterium.
                                                                                                                                                                            Unpublished
                                                                                                                                                                                            Disease in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                       /organism="Agrobacterium
/mol_type="genomic DNA"
/strain="C58"
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/function="DNA binding"
          /db_xref="taxon:176299"
                            isolate="Cereon"
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No. 2e-78;
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                                                                     tumefaciens
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>me, section 80
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complement (666 . 1073)
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                                                                                                                                                                                                                                                                                                                                                         3641. .4060 -
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Vibrio cholerae (group O1 strain N16961)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="AGR_C_1663"
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transl_table=11
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RESULT 11
AE009056
LOCUS
                                     KEYWORDS
SOURCE
                                                                                                                                  ACCESSION
                                                                                                                                                                                                       DEFINITION
                                                                                                       VERSION
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Best Local
      ORGANISM
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                                                                                                              Agrobacterium tumefaciens str. C58 of 256 of the complete sequence. AE009056 AE008688
Agrobacterium tumefaciens Agrobacterium tumefaciens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATGTTCATACTGCACTTTCTGGAACATCTGCTCCTGCTTCTGTTGCTGTTAACGTTGAG
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/transl_table=11
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                                                                                                       GI:17739283
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.8809
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77.4%;
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Pred. No. 2.9e-72;
                                                                                                                                                                                                    circular
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98195-7242, USA
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                               /gene="Atu0906"
1245. .1943
/gene="Atu0906"
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                                                                                                                                                                     PFCQECAAAL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="dskA"
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note="identified by sequence similarity; putative; ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="synonym:
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Wood, D. W., Setubal J.C., Kaul, R., Monks, D., Chen, L., Wood, G.E., Chen, Y., Woo, L., Kitajima, J.P., Okura, V.K., Almeida, N.F., Jr., Zhou, Y. B., Bovee, D. Sr., Chapman, P., Clendenning, J., Deatherage, G., Gillet, W., Grant, C., Guenthner, D., Kutyavin, T., Levy, R., Li, M., McClelland, E., Palmieri, A., Raymond, C., Rouse, G., McClelland, E., Palmieri, A., Gordon, D., Eisen, J.A., Paulsen, I., Saenphimmachak, C., Wu, Z., Gordon, D., Eisen, J.A., Paulsen, I., Karp, P., Romero, P., Zhang, S., Yoo, H., Tao, Y., Biddle, P., Jung, M., Krespan, W., Perry, M., Gordon-Kamm, B., Liao, L., Kim, S., Hendrick, C., Zhao, Z., Dolan, M., Tingey, S. V., Tomb, J., Gordon, M.P., Olson, M.V.
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Rhizobiaceae; Agrobacterium.
1 (bases 1 to 10229)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 294 (5550), 2317-2323 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /trānslation="MSLTRHAKWRIKPKETAMYKKIIVPVDLSATDKGEKILEKAKAL
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                                                                                                                                                                                                                                                                                                       note="identified by sequence similarity; putative; ORF ocated using Blastx/Glimmer"
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located using Blastx/Glimmer"
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/product="1d="Na+/H+ antiporter"
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2046. .2543
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/note="identified by sequence similarity; putative;
located using Blastx/Glimmer"
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/gene="Atu0908"
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HRGLGQKLLDSTIAIACGTGFALFLMRATQASFDNRLTDFYNTYSKVIAHGANVVNVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="identified by sequence similarity; putative; ocated using Blastx/Glimmer"
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note="identified by sequence similarity; putative; ORF ocated using Blastx/Glimmer"
                                                  gene="mnhB"
                                                                                                     note="synonym:
                                                                                                                           gene="mnhB"
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GATGTTCATACTGCACTTTCTGGAACATCTGCTCCTGCTTCTGTTGCTGTTAACGTTGAG 180
                              CCAGAGGAGTATAGAGAGAAGTGGGATCTTCCTGTTGATTACCCTATGGTTGCTCCTGCT 360
                                                                                                                                            GAGTGTGGTGGTTCTTTCAAGTCTCTCAAGCGTCACCTTACTACTCATCACTCTATGACT 300
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                                                                                        GAATGTGGCGGCTCGTTCAAGTCGCTGAAGCGGCATCTCACGACGCATCACAGCATGACG
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Conservative
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YALHSMVLMTALYLAAGHAARLGGGFSLTSLGDLYRQAPWFSALALALFFAGSGLPPF
SGFWPKAULVKSAIDIGAWHLAAAILVSGFIATIAFGRUFCAFPUTTSAGQDALQ
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QTDDTDEMRTAEPAGEPLPPLGY"
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alsiygiaygvtavrraivfhplsiagaglllamlsglvsmasgvpfmtglmvypslf
gvevplstvmsfdigvylvvvgaitsialaleeresd"
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/transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (28-NOV-1994) H.A. Hussain, University of East Anglia, School of Biological Sciences, Norwich NR4 7TJ, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pleiotropic effects of regulatory ros mutants of Agrobacterium radiobacter and their interaction with Fe and glucose Mol. Plant Microbe Interact. 8 (5), 747-754 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Johnston, A.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agrobacterium tumefaciens (Rhizobium radiobacter)
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X82941
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Hussain, H.A.
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                                                  GTTGCTGCTTACGTTTCTAACCACGTTGTTCCTGTTACTGAGCTTCCTGGACTTATCTCT 120
                                                                                                             ATGACTGAGACTGCTTACGGTAACGCTCAGGATCTTCTTGTTGAGCTTACTGCTGATATC
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                    GTGGCTGCCTATGTTAGCAACCACGTCGTCCCGGTAACGGAGCTTCCCCGGCCTTATTTCG
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ALSGTSAPASVAVNVEKQXPAVSVRKSVDHIVCLECGGSFKSLKRHLTTHHSWTPE
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276. .282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Agrobacterium tumefaciens"
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/strain="T1305 lac9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="rosAR"
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                                                                                                                                                                                                                                                                                                                                                                                                                       'note="similar to
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76.0%;
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                                                                                                                                                        Score 270; DB 15;
Pred. No. 9.5e-72;
0; Mismatches 105;
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Submitted (12-JUL-2004) General Microbiology, M.
University, Akademicka 19, Lublin 20-033, Poland
Location/Qualifiers
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Janczarek,M.B. and Skorupska,A.
rosR gene of Rhizobium leguminosarum
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Rhizobium leguminosarum bv. trifolii
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Janczarek, M.B. and
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                                                                                                                                                                                       /note="DNA binding protein; similar to Rhizobium etli Rosk, Agrobacterium tumefaciens Ros and Sinorhizobium meliloti MucR; regulator of exopolysacharide synthesis; member of Ros/MucR family of transcriptional regulators"
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                                                                                                                                                                                                                                                                                                                                                               /organism="Rhizobium leguminosarum
/mol_type="genomic DNA"
/strain="TA1"
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trifolii strain TA1 transcriptional
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Submitted (12-JUL-2004) General Microbiology, M.
University, Akademicka 19, Lublin 20-033, Poland
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1174 bp DNA linear BCT 11-AUG-2004
Rhizobium leguminosarum bv. trifolii strain 24.1 transcriptional
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Janczarek, M.B. and Skorupska, A.
rosk gene of Rhizobium leguminosarum
the exopolysaccharide production
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Rhizobium leguminosarum bv. trifolii
Bacteria, Proteobacteria; Alphaproteobacteria;
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Janczarek, M.B. and S
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                                                  /note="DNA binding protein; similar to Rhizobium etli Rosk, Agrobacterium tumefaciens Ros and Sinorhizobium meliloti MucR; regulator of exopolysaccharide synthesis; member of Ros/MucR family of transcriptional regulators"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTTGCTGCTTACGTTTCTAACCACGTTGTTCCTGTTACTGAGCTTCCTGGACCTTATCTCT
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TATGCCGAAGCGCGTTCGCGCCCTGGCAAAGGAGATGGGCCTCGGGCAGCGCCGCAAG
                                TACGCTGAGGCTCGTTCTCGTCTCGCTAAGGAGATGGGTCTCGGTCAGCGTCGTAAG 417
                                                                                                   CCGGAAGAATACCGCGAGAAGTGGGACCTGCCGACCGATTACCCGATGGTAGCGCCCCGCT
                                                                                                                                              CCAGAGGAGTATAGAGAGAAGTGGGATCTTCCTGTTGATTACCCTATGGTTGCTCCTGCT 360
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ALSNTSVPQPAAAIVEKQKPAVSVRKSVQDEQITCLECGGNFKSLKRHLMTHHSLSPE
EYREKWDLPTDYPMVAPAYAEARSRLAKEMGLGQRRKRGRG"
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69.3%;
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pred. No. 5.9e-54;
0; Mismatches 128;
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mucR gene; MucR protein; transcrip Sinorhizobium meliloti (Rhizobium Sinorhizobium meliloti Submitted (20-APR-1999) Rivilla R., de Madrid, Campus de Cantoblanco, M. producing Sinorhizobium Unpublished MucR does not repress Martin, M., Lloret, J., Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiaceae, Sinorhizobium. AJ237844.1 RME237844 Rhizobium meliloti mucR Direct Submission Rivilla,R. Rivilla,R. (bases 1 to 432) ) mol /gene="mucR" Location/Qualifiers function="putative transcriptional regulator" 'gene="mucR" country="Spain" db\_xref="taxon:382" strain="EFB1" organism="Sinorhizobium .432 GI:6465845 .432 type="genomic DNA" expE genes ım meliloti Sanchez-Contreras, M., gene, transcriptional regulator 432 bp DNA strain EFB1 expression ., Biologia, Universidad Madrid 28049, SPAIN meliloti) linear ä Bonilla, I. a galactoglucan Rhizobiales; BCT 21-NOV-1999 Autonoma

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361 TATGCGGAAGCCCGCTCGCGGCTCGCCAAGGAAATGGGTCTCGGACAGCGTCGTAAG 417
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/transI_table=11
/producT="MucR protein"
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ALNNTTAPAPVVVPVEKPKPAVSVRKSVQDDQITCLECGGTFKSLKRHLMTHHNLSPE
DYRDKWDLPADYPMVAPAYAEARSRLAKEMGLGQRRKRRGK"
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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64	64	89	94.4	94.4	199.4	199.4	291.6	291.6	291.6	317	317	317	458	458	458	458	458	Score
14.0	14.0	14.8	20.6	20.6	43.5	43.5	63.7	63.7	63.7	69.2	69.2	69.2	100.0	100.0	100.0	100.0	100.0	Query Match
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The present invention relates to a novel nucleic acid molecule encoding a ROS repressor protein optimised for plant codon usage and exhibiting ROS operator binding activity and/or ROS repressor activity. The nucleic acid molecule comprises a regulatory region operatively linked to a gene of interest and one or more ROS operator sequence capable of controlling the

New nucleic acid molecule encoding a ROS repressor, useful for controlling gene expression in plants, comprises a regulatory region operatively linked to a gene of interest and one or more ROS operator

Claim 2; Page 70; 84pp; English.

sequence.

WPI; 2003-148467/14.

Hannoufa A,

Hegedus D,

Bate N;

(MIAC ) CANADA DEPT AGRIC & AGRI-FOOD CANADA

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12.5			12.5		12.6						12.6	12.6	12.6	12.6	12.7	12.8	12.9	13.3	13.3	13.3	14.0	14.0	14.0	14.0	14.0	14.0
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ABN95250	ABK36100	ADX31923	ABZ12438	ABS15980	AAI08383	ABS41558	AAK16207	AAK41953	ABA34854	ABA49878	AAI48016	ABA67796	AAI22718	ADN97263	AAZ45602	ADQ67296	ADQ97348	ADN97265	ADN97258	ADN97264	ADN12162	AAV19941	AAV73805	ADV68153	ADJ65095	ABA93487
Abn95250 Gene #174	Abk36100 cDNA sequ	Adx31923 Plant ful	Arabido	Abs15980 Human gen	Aai08383 Probe #83	Abs41558 Human liv	Aak16207 Human bra	Aak41953 Human bon	Aba34854 Probe #13	Aba49878 Human bre	Aai48016 Probe #16	Human	Aai22718 Probe #12	Adn97263 AGC10 arr	Aaz45602 cDNA sequ	Adq67296 Novel hum	Adq97348 Mouse can	Adn97265 AGC10 rev	Adn97258 AGC10 STR	AGC10	Adn12162 Human her	Aav19941 KSHV long	Aav73805 KSHV LUR	Kapo	Adj65095 HHV8 DNA	Aba93487 Kaposi's

## ALIGNMENTS

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RESULT 1
AD52861
ID SAAD5
XX AAD5
XX AAD5
XX AAD5
XX AAD5
XX ROS
XX ROS
XX ROS
XX ROS
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AALS63C
AALS63C
AALS6
XX AALS
XX AALS
XX AALS
XX Gene
XW Gene
XW Gene
XW Unid
XX Unid
XX Unid
XX Unid
XX WO20
PN WO20
PP 21-N
XX 21-N
XX WALS
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                                                                                                                                                                               23-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene expression system; plant; ROS; vector; metabolic engineering; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAL56364 standard; DNA; 458
                                                                            Hannoufa A,
                                                                                                                            (MIAC ) CANADA MIN AGRIC & AGRI-FOOD.
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Pred. No. 2.7e-121;
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                                                                                                                                                        New nucleic acids encoding a ROS repressor optimized for plant codon usage and exhibits ROS operator binding activity, ROS repressor activity or both, useful for regulating gene expression in plants.
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91; Opp; English.

The present invention relates to a nucleic acid construct comprising a regulatory region operatively linked to a gene of interest and one or more ROS operator sequence capable of controlling the activity of the regulatory region which is functional in plants, encodes a ROS repressor optimised for plant codon usage and exhibits ROS operator binding activity, ROS repressor activity or both. The nucleic acid molecule or its derivative is useful for the regulation of gene expression in plants. The gene expression can be used in metabolic engineering to produce plants that accumulate large amounts of certain intermediate compounds. The present sequence is a polynucleotide used in constructs of the

Sequence 458 BP; 91 A; 105 C; 111 G; 151 T; 0 U; 0 Other,

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100.0%; Pred. No. 2.7e-121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid molecule encoding a ROS repressor, useful for controlling gene expression in plants, comprises a regulatory region operatively linked to a gene of interest and one or more ROS operator
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                  AACCGTCCAAAAAAGAAGCGTAAGGTCTGAGAGCTCGC
                                                                                                                                                                       GAGTGTGGTTGCTTTCAAGTCTCTCAAGCGTCACCTTACTACTCATCACTCTATGACT
                                                                                                                                                                                                                                AACCGTCCAAAAAAGAAGCGTAAGGTCTGAGAGCTCGC 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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/note= "Nuclear localisation signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 A; 110 C; 117 G; 153
                                                        CTCGTTCTCGTCTCGCTAAGGAGATGGGTCTCGGTCAGCGTCGTAAGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 458; DB 8;
Pred. No. 2.7e-121;
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ATGACTGAGACTGCTTACGGTAACGCTCAGGATCTTCTTGTTGAGCTTACTGCTGATATC ATGACTGAGACTGCTTACGGTAACGCTCAGGATCTTCTTGTTGAGCTTACTGCTGATATC

Matches Query Match

Local

Similarity

100

.08:

Score 458; Pred. No.

3; DB 12; 2.7e-121;

Length Indels

472; 0;

Gaps

0

60 74

100.0%;

0

Mismatches 458;

Conservative

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This invention relates to a novel method for regulating gene expression CC in transgenic plants using chromatin remodelling factors. Specifically, CC it comprises transforming a plant with one or more constructs comprising CC a first nucleotide sequence that is operably linked to a regulatory CC region and is capable of binding to a fusion protein, and a second CC nucleotide sequence that encodes said fusion protein. This fusion protein CC comprises a DNA binding protein (VP16 or GAL4), or a portion thereof, CC that can bind to and regulate expression of the gene of interest (i.e. CC the first polynucleotide) and a recruitment factor protein (BNSCL1 or CC invention describes the chromatin remodelling protein as a histone acetyl transferase (HAT) or histone deacetylase (referred to as either HD, HDA CC referably this protein is HDA19. As such, this method can be used to greferably this protein is HDA19. As such, this method can be used to by regulating the expression of a nucleic acid sequence of interest. This cC codon optimised for use in plants, used in an exemplification of the
 Sequence 472 BP;
                                                                                                                                                                                                                                                                                                                                                                     Regulating expression of a eukaryote and growing (
                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUN-2002; 2002US-0387088P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROS; ds; gene; transgenic plant; chromatin remodelling factor; DNA binding protein; VP16; GAL4; recruitment factor; BnSCL1; bnKCP1; histone acetyl transferase; HAT; histone deacetylase; HD; HDA; HDAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant codon optimised Agrobacterium tumefaciens
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92 A; 110 C;
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                                                                                                                                                                                                                                                                                                                                                                      a nucleic acid sequence of interest by providing the eukaryote.
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 117 G;
   153
 T; 0 U;
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                                                                                     Repressor-mediated plant selection strategies to identify transgenic plants comprising using a selectable marker system for plant transformation that is benigh to the plant and confers no advantage of the plantage of the pla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repressor-mediated plant selection; transgenic; antibiotic plant-optimised; Ros selectable marker; ds; gene.
                                                                                                                                                                                                                                                                                                                                                            03-OCT-2002; 2002US-0416369P
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                         Example 2;
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                      SEQ ID NO 1; 125pp; English
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/product= "Agrobacterium tumefaciens
selectable marker protein"
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                                                                                                                                                                                                                                                                                                                                                                 14-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACCGTCCAAAAAAGAAGCGTAAGGTCTGAGAGCTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACGCTGAGGCTCGTTCTCGTCTCGCTAAGGAGATGGGTCTCGGTCAGCGTCGTAAGGCT
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                                                                                                                                                                                                                                                                                                          tumefaciens ros repressor consensus
                                                                                                                                                                                              tumefaciens
                                                                                                                                                                                                                                                   protein; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; 110 C; 117 G;
                                                                                                                                                                                                                                                                                                                                                                   entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                   gene;
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                                                                                                                                                                Matches
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Best Local Similarity
                                                                                                                                                                                                                                 The present invention relates to a novel nucleic acid molecule encoding a ROS repressor protein optimised for plant codon usage and exhibiting ROS operator binding activity and/or ROS repressor activity. The nucleic acid molecule comprises a regulatory region operatively linked to a gene of interest and one or more ROS operator sequence capable of controlling the activity of the regulatory region that is functional in plants. They are useful in controlling gene expression in plants using a repressor protein and corresponding operator sequences. The present sequence is Agrobacterium tumefaciens ros repressor consensus DNA
                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid molecule encoding a ROS repressor, useful for controlling gene expression in plants, comprises a regulatory region operatively linked to a gene of interest and one or more ROS operator
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                                     GATGTTCATACTGCACTTTCTGGAACATCTGCTCCTGCTTCTGTTGCTGTTAACGTTGAG
                                                                    GTNGCNGCNTAYGTNWSNAAYCAYGTNGTNCCNGTNACNGARYTNCCNGGNYTNATHWSN
                                                                                                                               ATGACTGAGACTGCTTACGGTAACGCTCAGGATCTTCTTGTTGAGCTTACTGCTGATATC
                                                                                                                                                                                                             447 BP; 80 A; 53 C; 81 G;
 GAYGTNCAYACNGCNYTNWSNGGNACNWSNGCNCCNGCNWSNGTNGCNGTNAAYGTNGAR
                                                                                          GTTGCTGCTTACGTTTCTAACCACGTTGTTCCTGTTACTGAGCTTCCTGGACTTATCTCT
                                                                                                                 ATGACNGARACNGCNTAYGGNAAYGCNCARGAYYTNYTNGTNGARYTNACNGCNGAYATH
                                                                                                                                                                Conservative
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7; Mismatches 89
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cu This invention relates to a novel method for regulating gene expression in transgenic plants using chromatin remodelling factors. Specifically, constructs comprises transforming a plant with one or more constructs comprising careful for and is capable of binding to a fusion protein. This fusion protein comprises a DNA binding protein (VP16 or GAL4), or a portion thereof, that can bind to and regulate expression of the gene of interest (i.e. comprises a DNA binding protein (VP16 or GAL4), or a portion thereof, that can bind to and regulate expression of the gene of interest (i.e. conscience) that can bind to a chromatin remodelling protein. The present invention describes the chromatin remodelling protein. The present conscience is the first polymucleotide) and a recruitment factor protein. The present conscience is that the structure of chromatin, considered to a seither HD, HDA conscience is the HDA19. Which is required to alter the structure of chromatin, considered to a seither HD, HDA or HDAC), which is required to alter the structure of chromatin, considered the structure of chromatin, considered the services and phenotype e.g. to increase and a considered the appreciation of a considered to increase and a considered the constant of the present considered the structure of chromatin, considered the services and phenotype e.g. to increase and a considered the constant of a constant of
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DNA binding protein; VP16;
histone acetyl transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADI14225 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Regulating expression of a nucleic acid a eukaryote and growing the eukaryote.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MIAC ) CANADA DEPT
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; HAT; histone deacetylase; HD; HDA; HDAC;
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Best Local S
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                         WPI; 2004-035150/03
                                                                                                                                        04-DEC-2003
                                                                                                                                                                                                                     Gene expression
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                                                                                                                21-NOV-2002; 2002WO-CA001807
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                                                                                                                                                                                                                     system; plant; ROS; vector; metabolic engineering;
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nucleic acids encoding a ROS repressor optimized for plant

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Matches 260;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            usage and exhibits ROS operator binding activity, ROS repressor activity or both, useful for regulating gene expression in plants.
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   28-NOV-2002
                                                                                                              Agrobacterium tumefaciens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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58.3%;
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                                                                                                                                                                        expression; ds
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Pred. No. 9e-81;
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89; Indels
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a novel nucleic acid molecule encoding a ROS repressor protein optimised for plant codon usage and exhibiting ROS operator binding activity and/or ROS repressor activity. The nucleic acid molecule comprises a regulatory region operatively linked to a gene of interest and one or more ROS operator sequence capable of controlling the activity of the regulatory region that is functional in plants. They are useful in controlling gene expression in plants using a repressor protein and corresponding operator sequences. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid molecule encoding a ROS repressor, useful for controlling gene expression in plants, comprises a regulatory region operatively linked to a gene of interest and one or more ROS operator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Agrobacterium tumefaciens ros repressor DNA. Note: This sequence to encode the repressor protein shown as SEQ ID NO: 21 in page 76 specification. However this does not appear to be the case
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1;
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                                                                                                                                                                                                            GAGTGTGGTGGTTCTTTCAAGTCTCTCAAGCGTCACCTTACTACTCATCACTCTATGACT
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                                                                                                                                                                                                                                                                                                                          GATGTTCATACTGCACTTTCTGGAACATCTGCTCCTGCTTCTGTTGCTGTTAACGTTGAG
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                                                                                       TACGCTGAGGCTCGTTCTCGTCTCGCTAAGGAGATGGGTCTCGGTCAGCGTCGTAAGGCT
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                          AACCGT
                                                          TATGCCGAAGCCCGT
                                                                                                                     CCGGAAGAATATCGCGAAAAATGGGATCTGCCGGTCGATTATCCGATGGTTGCTCCCGCC
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standard; DNA; 429

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Matches 342;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acids encoding a ROS repressor optimized for plant codon usage and exhibits ROS operator binding activity, ROS repressor activity or both, useful for regulating gene expression in plants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 90-91; Opp; English.
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                                                                                                                 GATGTTCATACGGCACTCAGCGGAACATCGGCACCGGCATCGGTGGCGGTCAATGTTGAA
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                                                                                       GAATGTGGTGGCTCGAAGTCGCTCAAACGCCACCTGACGACGCATCACAGCATGACG
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CCGGAAGAATATCGCGAAAAAATGGGATCTGCCGGTCGATTATCCGATGGTTGCTCCCGCC
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Pred. No. 1.
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smatches 84;
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Matches Query Match Best Local

al Similarity 342; Conserv

Conservative

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Mismatches

Indels Length

Gaps

0

60

63.7**%;** 80.3**%**;

Score 291.6; Pred. No. 1.8 126 G;

DB 12;

429; 0,

Sequence

429

BP;

94

A; 115 C;

94 T; 0 U; 0

Other;

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XX ADR222
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                                                                                may be used for selecting transgenic plants, cells, tissue or entire plants which comprise a coding region of interest. The methods are not based on antibiotic resistance, are simple to carry out and provide a selectable marker system for plant transformation that is benign to the transformed plant and confers no advantage to other organisms in the event of gene transfer. The methods involve stringent selection of transformed cells and use an inexpensive and effective selection agent that is non-toxic to plant cells. The current sequence is that of the Agrobacterium tumefaciens wild-type Ros selectable marker DNA of the
                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel repressor-mediated plant selection strategies to identify and select plants, cells, tissue or entire plants which comprise a coding region of interest. The methods of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repressor-mediated plant selection strategies to identify transgenic plants comprising using a selectable marker system for plant transformation that is benign to the plant and confers no advantage to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; SEQ ID NO 19; 125pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "Agrobacterium tumefaciens wild-type
selectable marker protein"
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RESULT 12
AAV30458_0
WP Sequence split into 6
WP Fragment Name
AAV30458_0
WP AAV30458_1
WP AAV30458_5
ID AAV30458;
XX AV30458;
AC AAV30458 standard;
AC AAV30458;
XX AV30458;
CD Rhizobium species p
XX Symbiosis; open rea
KW degradation; metabc
XX 1egume; plant; ds.
XX 1egume; plant; ds.
XX 7egume; plant; ds.
XX 1egume; plant; ds.
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                                                                                                                                                                                                                                                                                                                                                  Symbiosis; open reading frame; ORF; plasmid; vector; transportation; degradation; metabolism; host range; nitrogen fixation; nodulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV30458 standard; DNA; 534720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCAGAGGAGTATAGAGAGAGAGTGGGATTGCTTCCTGTTGATTACCCTATGGTTGCTTCCTGCT
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                                                                                                                                                                                                                                                 Location/Qualifiers
417796. .418671
                                                                                                                                                                /standard_name= "ORF K1"
/product= "oligopeptide permease"
/note= "homologous to the OppC gene"
/18673. .419680
   /standard_name= "ORF K3"
/product= "oligopeptide permease"
/note= "homologous to the OppF ges
420774. .422159
                                                                                 /standard_name= "ORF K2"
/product= "oligopeptide permease"
/note= "homologous to the OppD ger
/19677. .420738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /standard_name= "ORF K8"
/product= "glutamate dehydrogenase-like protein"
/note= "homologous to the GLUD1 gene"
complement (430538. .431284)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /standard_name= "ORF K6"
/product=""(semi)aldehyde_dehydrogenase-like_protein"
/cmp_ement(426949. .428028)
                                                                                                                                                                                                                                                 genes"
                                                                                                                                                                                                                                                                                                                                                    /product= "protein involved biosynthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                /standard name= "ORF K13"
/product= "ferrodoxin/ferrodoxin-like
/note= "homologous to the FdxN gene"
complement(434753. .436234)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /standard_name= "ORF K12"
/product= "protein of unknown complement(434517. .434711)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /standard_name= "ORF K11"
/product= "protein of unknown function"
/note= "homologous to the FixU gene"
complement (434107. . . 434433)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /standard_name= "ORF K9"
/product= "transposase homologue"
complement(431296. .432840)
               /standard_name=
/gene= "fixB"
                                                                   /product= "protein required complement (439923. .441032)
                                                                                                                                                 /product= "protein required
complement(438605. .439912)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "homologous to the Inp complement (433880. .434110)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          428292.
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                                                                                                                                                                                                                                                                                                                                   complement (436460. .438130)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /standard_name= "ORF K7"
/product= "transposase homologue"
/note= "homologous to the Tnp gene"
428292. .429623
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/standard name= "ORF K4"
/product= "encapsulation-like protein"
/note= "homologous to the CapA gene"
                                                                                                gene= "fixC"
                                                                                                                                                                                /gene= "fixX"
                                                                                                                                                                                                                                                                                                  standard_name=
                                                                                                                                                                                                                                                                                                                                                                                   /gene= "nifB"
                                                                                                                                                                                                                                                                                                                                                                                                      /standard
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/product= "transposase homologue"
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                                                                                                                                                                                                    name= "ORF K16"
                                                                                                                     name=
   "protein required for nitrogenase activity"
                                                                                                                                                                                                                                                                   "positive regulator
                                                                                                                                                                                                                                                                                                                                                                                                      name= "ORF
                                      "ORF K18"
                                                                                                                                                                                                                                                                                                     "ORF
                                                                                                                     "ORF K17"
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 /standard_name= "ORF L10"
/product= "protein of unknown function"
/note= "homologous to the NifX gene"
459579. .460067
/*tag= ag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "C4-dicarboxylate transport protein" /note= "homologous to the DctAI gene" 446599. .447843
                                                                                                                                  /standard_name= "ORF
/product= "protein ir
biosynthesis"
                                                                                                                                                                                                                                                                                                                                                                       /standard_name= "ORF L6"
/gene= "nIfD"
/product= "alpha-subunit
/product= "454590. .456131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /standard_name= "ORF L3"
/product= "putative protein with
450341. .451396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "homologous to the 448497. .450203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /standard_name= "ORF L1"
/product= "cytochrome P450-like protein"
/note= "homologous to the CamC gene"
447844. .448500
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function"
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complement(442316. .442636)
                                                                                                  459093.
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                                                                                                                                                                                                                              biosynthesis"
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/*tag= ab
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/gene= "fixA"
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                                                                                                                                                                                                                                                                                                         /standard_name= "ORF L7"
/gene= "nifk"
/product= "beta-subunit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /standard_name= "ORF K22"
/product= "ferrodoxin-like protein"
/note= "homologous to the NifQ gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /standard_name= "ORF L4"
product= "luciferase alpha-subunit-like
roote= "homologous to the LuxA gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'standard_name= "ORF L2"
product= "gamma-hexachlorocyclohexane-dechlorinase-like
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product= "protein of unknown function"
                                                                                                                                                                                                                                           standard_name= "ORF L8"
product= "protein involved
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RESULT 13
AAV30459 0
WP Sequence split into 6
WP AAV30459 0
WP AAV30459 1
WP AAV30459 2
WP AAV30459 5
ID AAV30459 5
ID AAV30459;
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AC AAV30459;
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AC AAV30459;
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AC AAV30459;
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AC SANUL-1999 (first XX
AC AAV30459;
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AC G-JUL-1999 (first XX
AC AAV30459;
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Best Local Similarity
Matches 281; Conserv
                                                                 Symbiosis; open reading frame; ORF; plasmid; vector; transportation; degradation; metabolism; host range; nitrogen fixation; nodulation;
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nilarity 67.4%;
Conservative
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/product= "protein of unku
463201. .464739
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/product= "protein similar to
nitrogenase"
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/product="protein of unknown function"
/60501. .460920
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/standard_name= "ORF L14"
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16340 180 16280 120

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RESULT 14
AAV30458 3/c
Continuation (4 of 6) of A
WP Sequence split into 6 f
WP Fragment Name
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Best Local S
Matches 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated symbiotic plasmid from Rhizobium sp. NGR234 - used to develop products for modifying plant characteristics, e.g. nitrogen fixation, synthesis of compounds and stress response.
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20-MAY-1997;
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                                                                                                               TACGCTGAGGCTCGTTCTCGCTAAGGAGATGGGTCTCGGTCAGCGTCGTAAG
                                                                                                                                                                    CCAGAGGAGTATAGAGAGAAGTGGGATCTTCCTGTTGATTACCCTATGGTTGCTCCTGCT
                                                                                                                                                                                                                                 GAGTGTGGTTGTTTCAAGTCTCTCAAGCGTCACCTTACTACTCATCACTCTATGACT
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97GB-00010395.
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 AAV30458 from base 300001 fragments LOCUS AAV30458 Begin End
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Pred. No. 4.5e-46;
0; Mismatches 136;
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                 (Rhizobium species plasmid pNGR234a. Accession Aav30458
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RESULT 15
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CCTTACTCATCACTCTATGACTCCAGAGGAGTATAGAGAAGTGGGATCTTCCTGT
                            GACCGCAGACTTCATCATATGCCTGGAGGACGGTAAAAAATTCAAATCGCTGAAGCGACA
                                                                                        CAAGGCTGAGGAGGCTGCCGTCGAAGAACAGCGGCCCGCCGTCCCGATCAAGAAGTCAGT
                                                                                                                                                  CGATCTGGCCAGTCTTATTCAGCAGACGTATCTCTCGCTATGCAGCACCTCTCAGGCAGA
                                                                                                                                                                               TGAGCTTCCTGGACTTATCTCTGATGTTCATACTGCACTTTCTGGAACATCT---GCTCC
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Match
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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BH182027 020 K 19-
AL618977 T3 end of
AY325173 Rattus no
BH209707 Sm1-41.P23
DT996364 CNB184 A0
CB521826 UI-M-GH0-
BH184140 024 J 22-
AL62103 T7 end of
AZ65003 TM0520C01
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BF329437 CH230-235
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RESULT 1

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12.6	12.6		12.6	12.6	12.6		12.7				12.7	12.7	12.8			12.8		12.9		13.0	13.0		13.0		13.1
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BH200321 Sm1-50020	BX078177 BX078177	CZ285019 cp38h09.r	CZ280852 cp13g01.r	CK183608 EST772923	DW586149 PMAM-aaa2	Z90761 F.rubripes	AL243904 Tetraodon	BJ439038 BJ439038	BJ403974 BJ403974	BZ284533 CH230-385	CO543707 LyEST1134	BW478868 BW478868	DE235981 Trifolium	CA743784 wrils.pk0	AL199074 Tetraodon	DE214279 Trifolium	DW609105 CGX199-A0		CB181190 AGENCOURT	BI525376 602924305	BY706450 BY706450	BM247568 K0803H04-	BH211305 Sm1-50G22	BJ370460 BJ370460	CO041542 UI-M-FO0-

IGIN  24.9%; Score 114; DB 11; Length 401;  Best Local Similarity 65.8%; Pred. No. 2.4e-21;  Matches 196; Conservative 0; Mismatches 100; Indels 2; Gaps	ORIGIN  Query Match  Best Local of the second of the second of the second or
/organism="Rhizobium sp. NGR234" /mol_type="genomic DNA" /strain="ANU265" /db_xref="taxon:394" /clone="07e12" /clone="07e12" /clone lib="Shot-gun genomic library of Rhizobium strain ANU265" ANU265" pNGR234a"	
Haboratoire de Biologie Moleculaix University of Geneva 1 Chemin de l'Imperatrice, Chambes Tel: +44(0)1603450000 Fax: +44(0)1603450045 Email: virginie.viprey@bbsrc.ac.uk Class: shotgun. Class: shotgun. 1401	FEATURES SOUTCE
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium.  1 (bases 1 to 401)  1 (bases 1 to 401)  Viprey, V., Rosenthal, A., Broughton, W.J. and Perret, X. Genetic snapshots of the Rhizobium species NGR234 genome Genome Biol. 1 (6), RESEARCH0014 (2000)  11178268  Contact: Virginie Viprey	REFERENCE AUTHORS TITLE JOURNAL PUBMED COMMENT
AZ577265 07e12 Shot-gun genomic lii sp. NGR234 genomic clone   AZ577265 AZ577265.1 GI:11603506 GSS. Rhizobium sp. NGR234 Rhizobium sp. NGR234	AZ577265 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM

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Contact: Virginie Viprey
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University of Geneva
1 Chemin de l'Imperatrice, Chambesy/Geneva 1292, Switzerlan
Tel: +44(0)1603450000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viprey, V., Rosenthal, A., Broughton, W.J. and Perret, X. Genetic snapshots of the Rhizobium species NGR234 genome Biol. 1 (6), RESEARCH0014 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhizobium sp. NGR234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ577928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhizobiaceae, Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhizobium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ577928.1 GI:11604694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16e11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTGCTGCTTACGTTTCTAACCACGTTGTTCCTGTTACTGAGCTTCCTGGACTTATCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGACTGAGACTGCTTACGGTAACGCTCAGGATCTTCTTGTTGAGCTTACTGCTGATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGAATGCGGCGGGTACGTTCAAATCGCTGAAGCGCCATTTGATGACCCACCACAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAGTGTGG-TGGTTCTTTCAAGTCTCTCAAGCGTCACCTTACTACTCATCACTCTAT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGCCGAAGCCGGCGGGTTTCCGTTCGCAAGTCGGTGCAGGACGACCAGATCACTTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATGTTCATACTGCACTTTCTGGAACATCTGCTCCTGCTTCTGTTGCTGTTAACGTTGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTGCCGCCTACGTGAGCAACCACGTGGTTCCGGTTGCCGAGCTGCCGACGCTGATTGCC
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CTGCTCCTGCTTCTGTTGCTGTTAACGTTGAGAAGCCAGAAGCCTGCTGTTTCTGTTTCGTA 208
                                                                                                                                  AGGATCTTCTTGTTGAGCTTACTGCTGATATCGTTGCTGCTTACGTTTCTAACCACGTTG 88
                                                TTCCGGTTGCCGAGCTGCCGACGCTGATTGCCGACGTTCATTCGGCGCTCAACAATACAA 178
                                                                              TICCIGITACIGAGCITCCIGGACITATCICIGATGITCATACIGCACITICIGGAACAI 148
                                                                                                                ACGAACTCCTGGTTGAGCTGACGGCGGAAATCGTTGCCGCCTACGTGAGCAACCACGTGG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 Shot-gun genomic library of Rhizobium NGR234 genomic clone 16e11, genomic surv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 257)
                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      virginie.viprey@bbsrc.ac
                                                                                                                                                                                                                                                             /note="Vector: M13; derivative
pNGR234a"
                                                                                                                                                                                                                                                                                             /clone lib≈"Shot-gun genomic library of Rhizobium strain
ANU265™
                                                                                                                                                                                                                                                                                                                                                                        /organism="Rhizobium sp.
/mol type="genomic DNA"
                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:394"
/clone="16e11"
                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic
/strain="ANU265"
                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                             20.9%;
                                                                                                                                                                                           Score 95.6; DB Pred. No. 4e-16;
                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                           DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear GSS 08-DEC-2000 bium strain ANU265 Rhizobium survey sequence.
                                                                                                                                                                                                                                                                            strain of NGR234 cured
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                                                                                                                                                                                                           Length
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Best Local Similarity
                                                                                                                                              Matches
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                  345
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BH202231
                  ATGCTGCCGCTGCTTATGATGCTGCTGCTAATGCTGATGCTGCTGCTGCTGTTGATGATC
                                              CTGCTTACGTTTCTAACCACGTTGTTCCTGTTACTGAGCTTCCTGGACTTATCTCTGATG
                                                                              CTGCTGTTGCTGCTGATGCTGATGCTAATGCTGATGCTGCTGCTGCTGATGATGATG
                                                                                                             CTGAGACTGCTTACGGTAACGCTCAGGATCTTCTTGTTGAGCTTACTGCTGATATCGTTG
                                                                                                                                              Conservative
                                                                                                                                                             14.2%;
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: nelsayed@tigr.org
Clones are derived from the Schistosoma mansoni (Puerto Rico)
BAC library. For clone availability, please contact Dr. Najib
El-Sayed at TIGR (nelsayed@tigr.org) or Dr. Phillip LoVerde at
State University of New York, Buffalo, New York, USA
(loverde@buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schisto
1 (Dases 1 to 782)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2001)
Other_GSSs: Sm1-61C12.TF
Contact: Najib M. E1-Sayed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: M13 Rev
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of end sequences from Schistosoma mansoni (Puerto Rico strain)
Sml BAC library for gene discovery and map construction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shetty, J., Simpson, A., Malek, J., Koo, H., LoVerde, P.T. and El-Sayed, N.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schistosoma mansoni
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GSS.
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/clone libe "Sml"
/clone "Vector: pBeloBAC11; Site 1: Hin dIII; Constructed
/note="Vector: pBeloBAC11; Site 1: Hin dIII; Constructed
in the laboratory of Dr. Denis Le Paslier at the Fondation
in the laboratory of Dr. Denis Le Paslier at the Fondation
Jean Dausset (EPH, Paris, France. Briefly, Schistosoma
mansoni agarose embedded DNA was partially digested with
Hin dIII. High molecular weight fragments were ligated in
pBeloBAC11 digested with Hin dIII. The average insert size
is 100 kb. Total clone coverage: approx. 7.95 x the
haploid genome. Further information can be found in Le
Paslier et al. (2000) Construction and characterization of
a Schistosoma mansoni bacterial artificial chromosome
library. Genomics 65: 87-94."
                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="Puerto Rico"
/db_xref="taxon:6183"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Schistosoma mansoni"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                             /clone="Sm1-61C12"
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ni genomic clone Sm1-61C12,
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Score 65.2; DB Pred. No. 2.7e-0; Mismatches

DB 11; 2.7e-07; hes 113;

Indels Length

<u>,</u>

Gaps

286 124 346 64 0 782;

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RESULT 4
BM588321/c
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Contact: Holt R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   711 bp mRNA linear EST 25-
17000687322518 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA
19600449697628 5', mRNA sequence.
BM588321
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Seq primer: M13 Reverse.
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45 w. Gude Dr., Rockville,
Tel: 2404533151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Anophelinae; Anopheles.
1 (bases 1 to 711)
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                                                        TTCATACTGCACTTTCTGGAACATCTGCTCCTGCTTCTGTTGCTGTTAACGTTGAGAAGC
                                                                                                                                                           CTGCTTACGTTTCTAACCACGTTGTTCCTGTTACTGAGCTTCCTGGACTTATCTCTGATG
                                                                                                                                                                                                                                      CTGAGACTGCTTACGGTAACGCTCAGGATCTTCTTGTTGAGCTTACTGCTGATATCGTTG
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CATCTGCTGTTGCTGCATCTGCTGTTGTTGCTGCTGTTGCTGCTGCTGCTGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="A.Gam.ad.cDNA.blood1"
/note="Vector: pSport1; Site 1: Sal1; Site 2: Not1; Whole adult mosquitoes (mixed sex) Frozen on liquid nitrogen 24 hours after human blood feeding. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and column of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="19600449697628"
/dev_stage="Adult"
/lab_host="DH10b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'mol_type="mRNA"
/strain="RSP-ST (Reduced susc.
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                                                                                                                                                                                                                                                                                                                                                                                  14.0%;
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Pred. No. 5.7e-07;
0; Mismatches 190
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RESULT 5
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Best Local
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 66
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USDA/ARS and Department of Agronomy
Kansas State University
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Nylon Filter Arrays Reveal Differential Expression
Sequence Tags in Wheat Roots Under Aluminum Stress
J. Integr. Plant Biol. 47 (7), 839-848 (2005)
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CF569196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF569196 581 bp mRNA linear EST 08-SEP-2004 EST057 Subtracted, Clontech (cat. # K1804-1) Triticum aestivum cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: gbai@bear.agron.ksu.edu
Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Pooideae; Triticeae; Triticum.
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                                                TCATACTGCACTTTCTGGAACATCTGCTCCTGCTTGTTGCTGTTAACGTTGAGAAGCA 185
                                                                                         TGCTTACGTTTCTAACCACGTTGTTCCTGTTACTGAGCTTCCTGGACTTATCTCTGATGT
                                                                                                                                                      TGAGACTGCTTACGGTAACGCTCAGGATCTTCTTGTTGAGCTTACTGCTGATATCGTTGC
                              (bases 1 to 581)
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence stop: 581
                                                                                                                                                                                                                                                                                          /tissue_type="root"
/clone_Tib="Subtracted, Clontech (cat. # K1804-1)"
/note="BSD" from wheat (Triticum aestivum, cv. OK910
root in response to aluminum stress"
                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/cultivar="OK91G106"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                organism="Triticum aestivum"
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Pred. No.
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RESULT 7
AY383694/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (20-FEB-2004) Sanger Centre, Hinxton, CB10 1SA, UK. http://www.sanger.ac.uk/MICER Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams, D.J., Biggs, P.J., Cox, A.V., Jonkers, J., Smith, J., Plumb, R.W., Rogers, J. and Bradley, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CR237539.1 GI:50016388
GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
  AY383694
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                                                                    CIGCIGCICCIGCICCIGCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN177k02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone_lib="MHPN"
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Pred. No. 1.1e-06;
0; Mismatches 200
969
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Taylor,R.G.,
mRNA
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linear
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Nishijima,I., Yu,Y.,
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RESULT 8 BH182027/c LOCUS

DEFINITION

BH182027 723 bp 020\_K\_19-rev SmBAC1 Schistosoma genomic survey sequence.

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linear genomic cl

gr GSS 19-OCT-2001 clone 020K19 5',

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1 (bases 1 to 963)

Xu,C.S., Chang,C.F., Han,H.P., Wang,G.P., Chai,L.Q., Yuan,J.Y., Yang,K.J., Zhao,L.F., Ma,H., Wang,L., Wang,S.F., Xing,X.K., Shen,G.M., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.B. Liver regeneration after PH
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (09-SBP-2003) Henan Bioengineering Key Lab, Henan Normal University, No. 148 Jianshe Road, Xinxiang City, Henan 453002, P.R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus LRRGT00039 mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus
                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                     TGATGTTGTTGTTGTTGCTGTTGTTGATGTTGCTGTTATTGCTGTTGTTACTGT
                                                                                TGCACTTTCTGGAACATCTGCTCCTGCTTCTGTTGCTGTTAACGTTGAGAAGCAGAAGCC
                                                                                                                                                                                                          CGTTTCTAACCACGTTGTTCCTGTTACTGAGCTTCCTGGACTTATCTCTGATGTTCATAC
                               TTCTTTCAAGTCTCT
                                                            TACTGTTGTTATTGCTGCTGTTGTTGCTGTTGCTGTTGTTATTGCTGTTGTTGC
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TGTTGTTATTGCTGT
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                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        /strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Rattus norvegicus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                            ITTATSTTATTTTSITTTATAITTTATATTTATATTAIATKQQ'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="LRRGT00039"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="liver regeneration-related"
                                                                                                                                                                                                                                                                                                                            13.8%;
                             266
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                                                                                                                                                                                                                                                                                                              Score 63; DB 6; Li
Pred. No. 1.2e-06;
0; Mismatches 120;
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                                     246
                                                                            126 TCATACTGCACTTTCTGGAACATCTGCTCCTGCTTCTGTTGCTGTTAACGTTGAGAAGCA
                                                                                                                                                                                                                                      223
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Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

1 (bases 1 to 723)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: M13 reverse primer Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Institut Pasteur de Lille
1 rue du Professeur A. Calmette, 59019.
Tel: (33) (0)3 2087783
Fax: (33) (0)3 20877888
Email: Raymond Dierce@pasteur-lille.fr
CNS sequencing ID-DGOAM20AF10BP1
Plate: 020 row: K column: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Other_GSSs: 020_K 19-21
Contact: Pierce_RJ
INSERM U 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bacterial artificial chromosome library Genomics 65 (2), 87-94 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Le Paslier,M.C., Pierce,R.J., Merlin,F., Hirai,H., Wu,W., Williams,D.L., Johnston,D., LoVerde,P.T. and Le Paslier,D. Construction and characterization of a Schistosoma mansoni
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BH182027.1
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                                     TGGTGGT 252
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TGATGAT 37
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab host="Biomphalaria glabrata"
/clone lib="SmBAC1"
/note="Vector: pBeloBAC 11; Site 1: Hind III; Partially
/indt III digested and size-selected S. mansoni cercarial
DNA was ligated into Hind III digested pBeloBAC 11 vector
and used to transform E. coli DH10B. The complete library
contains 23808 clones from 4 independent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sizing-ligation-transformations. Average insert size
ranges from 70-127 kb and genome coverage is 7.9-fold."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Schistosoma mansoni"
/mol_type="genomic DNA"
/strain="Puerto-Rican"
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                                                                                                                                                                                                                                                                                                                                                                                                                 13.7%;
                                                                                                                                                                                                                                                                                                                                                                                              Score 62.6; DB 11;
Pred. No. 1.4e-06;
1; Mismatches 115;
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RESULT

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RESULT 10
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Direct Submission

Direct Submission

Submitted (05-OCT-2001) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

Partially Hind III digested and size-selected S. mansoni cercarial

DNA was ligated into Hind III digested pBeloBAC 11 vector and used

to transform E. coli DH10B. The complete library contains 23808

clones from 4 independent sizing-ligation-transformations. Average

insert size ranges from 70-127 kb and genome coverage is 7.9-fold.
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AL618977.1
GSS.
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1 (bases 1 to 723)

Le Pasller,M.C., Pierce,R.J., Merlin,F., Hirai,H., Wu,W., Williams,D.L., Johnston,D., Loverde,P.T. and Le Paslier,D. Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library

Genomics 65 (2), 87-94 (2000)
AY325173 1933 bp.
Rattus norvegicus Aa2-050 mRNA,
AY325173
AY325173.1 GI:33086523
HTC.
Rattus norvegicus (Norway rat)
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/note="end : T3"
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/clone="020AF10"
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/strain="Puerto-Rican"
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53.0%;
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Pred. No. 1.4e-06;
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                                                                       complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

1 (bases I to 1933)

1 (Chases I to 1933)

1 (Chases I to 1933)

2 (Chai, L., Wang, L., Wang, K.J., Yan, H.M., Chang, C.F., Zhao, L.F., Ma, H., Wang, L., Wang, S.F., Han, H.P., Wang, G.P., Chai, L.Q., Yuan, J.Y., Shi, J.B., Rahman, S., Wang, Q.N. and Zhang, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 1933)
Xu,C.S., Li,W.Q., Li,Y.C., Yang,K.J., Yan,H.M., Chang,C.F.,
Zhao,L.F., Ma,H., Wang,L., Wang,S.F., Han,H.P., Wang,G.P.,
Chai,L.Q., Yuan,J.Y., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.B.
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TCGTTCTCGTCTCGCT 387
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                                                                                                                                                                                                    TTCTTTCAAGTCTCTCAAGCGTCACCTTACTACTCATCACTCTATGACTCCAGAGGAGTA 311
                                                                                                                                                                                                                                                                                          TAGAGAGAAGTGGGATCTTCCTGTTGATTACCCTATGGTTGCTCCTGCTTACGCTGAGGC 371
                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAP92574.1"
/db_xref="GI:33086524"
/translation="MAAGLDQGPARCAGAGPGPPLLLRDSILAFVLQMTGSNEPKLN
/translation="MAAGLDQGPARCAGAGPGPPLLLRDSILAFVLQMTGSNEPKLN
OPPEDGISSVLEPSPMTSQPFLLVSSWDTSVRLYDVPANSMRLKYQHTGAVLDCAFYVEN
LVGTHDAPIRCVEYCPEVNVMVTGSWDDTVKLWDPRTPCNAGTTSQPEKGYVLSSIEG
RVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNAISLSQYPQHICHSNDGTTLA
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AVGLMSSRIFVLTIPPSADTAKRQAFLDIAHVCYSKATTAVTLVASMHKSTTGV
ITLLVFVTTYLMRSTIKERSLLLLVVKGGKVHGGEGKSGSPKSQKHFLLALQPFIMH
NSNSNNNNNSNNNNSNNNNSNNNNSNSNSSSSNSTSNNSNSNSNSN
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/mol_type="mRNA"
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Pred. No. 2.1e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: nelsayed@tigr.org
Clones are derived from the Schistosoma mansoni (Puerto Rico)
Elones are contact Dr. Najib
BAC library. For clone availability, please contact Dr. Najib
El-Sayed at TIGR (nelsayed@tigr.org) or Dr. Phillip Loverde at
State University of New York, Buffalo, New York, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schistosoma mansonı
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BH209707.1 GI:16388592
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: M13 For Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sml BAC library for gene 
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (loverde@buffalo.edu)
AGAAGCCTGCTGTTTCTGTTCGTAAGTCTGTTCAGGATGATCATATCGTTTGGTTTGGAGT
                                                                                                                                  CTGCTGCTGATGCTGCTGATGATGCTGCTGCTGCTGATGCTGCTGATGATGCTG
                                                                                                                                                                         CTGCTTACGTTTCTAACCACGTTGTTCCTGTTACTGAGCTTCCTGGACTTATCTCTGATG
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                                             CTGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGATGATGATGATGATG
                                                                                  TTCATACTGCACTTTCTGGAACATCTGCTCCTGCTTCTGTTGCTGTTAACGTTGAGAAGC
                                                                                                                                                                                                                     CTGATGCTGCTGCTGATGATGATGATGCTGCTGCTGCTGATGATGATGATGATCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBeloBAC11; Site 1: Hin dIII; Constructed in the laboratory of Dr. Denis Te Paslier at the Fondation Jean Dausset, CEPH, Paris, France. Briefly, Schistcosoma mansoni agarose embedded DNA was partially digested with Hin dIII. High molecular weight fragments were ligated in pBeloBAC11 digested with Hin dIII. The average insert size is 100 kb. Total clone coverage: approx. 7.95 X the haploid genome. Further information can be found in Le Paslier et al. (2000) Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library. Genomics 65: 87-94."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="Puerto Rico"
/db_xref="taxon:6183"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Sm1"
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53.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expressed sequence tags from Gasterosteus aculeatus Unpublished (2003) Contact: Grimwood, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes; Gasterosteidae; Gasterosteus.
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Gasterosteus aculeatus
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DT996364
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Plate: 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kingsley, D.M., Peichel, C., Balabahdra, S., Schmutz, J. and Myers, R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 650 320 5801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence stop: 865.
                                                                                                                                           /lab_host="blue" (TI phage resistant)"
/clone lib="SHGC-CNB"
/clone lib="SHGC-CNB"
/note="Vector: Express 1; Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a cDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic NotI site (first strand primer: '-GACTAGTTCTAGATCGCGAGCGCCC(T)25-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5 prime end of mRNA, and cloned directionally into the NotI and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxATC' (where is ATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at:

http://www.openbiosystems.com/cdna_library_construction_fa
q.php#8 The primary_library_was_transformed_and_amplified
in_DH10B_(TI_phage_resistant)_bacteria. Clones_available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               quality sequence start: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            California Ave, Palo Alto, CA 94304, USA
550 320 5917
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                                                                                                       http://www.openbiosystems.com/stickleback"
                                                                                                                                     from Open Biosystems:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="CNB184-A03"
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/db_xref="taxon:69293"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'sex="mixed male and female'
  13.4%; 55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            type="mRNA"
  Score 61.6; DB 10;
Pred. No. 3.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of Medicine
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                         Length 1429;
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UI-M-GH0-ceo-a-21-0-UI.r1 NIH_BM
IMAGE:6842110 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mousefl.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Novel Contac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMAGE: 6842110
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1. (bases 1 to 747)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence: 289-410, >(CAA)n#Simple_repeat 406-531,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The following repetitive elements were found in this cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAAGCCTGCTGTTCTGTTCGTAAGTCTGTT 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGAGACTGCTTACGGTAACGCTCAGGATCTTCTTGTTGAGCTTACTGCTGATATCGTTG 64
                                                                                                                   /tissue_type="Whole brain"
/dev_stage="1, 5, and 15 days newborn"
/lab_host="DH108 (T1 phage resistant)"
/lab_host="DH108 (T1 phage resistant)"
/clone lib="NIH BMAP GH0"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
/site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Duble strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail is CGAACTGAAT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="IMAGE:6842110"
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/strain="C57BL/6"
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Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

1 (bases 1 to 482)
1 (bases 1 to 482)
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Seq primer: M13 -21 primer
Class: BAC ends
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1 rue du Professeur A. Calmette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Other GSSs: 024 J 22-rev
Contact: Pierce RJ
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BH184140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: Raymond.Pierce@pasteur-lille.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INSERM U 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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(33) (0)3 20877888
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            program coordinator.
                                                                                                                                                              /mol_type="genomic DNA'
/strain="puerto-Rican"
/db_xref="taxon:6183"
/dev_stage="cercariae"
/lab_host="Biomphalaria
/clone_lib="SmBAC1"
                                                                                                                                   clone="024J22"
                                                                                                                                                                                                                                                                organism="Schistosoma
                                                                                                        Bex="mixed"
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0; Mismatches
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mansoni genomic clone 024J22 5',
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ORGANISM
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Best Local Similarity
Matches 131; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                l (bases 1 to 482)
Le Paslier,M.C., Pierce,R.J., Merlin,F., Hirai,H., Wu,W.,
Williams,D.L., Johnston,D., LoVerde,P.T. and Le Paslier,D.
Construction and characterization of a Schistosoma mansoni
bacterial artificial chromosome library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNS07P5F 482 bp DNA line
T7 end of clone 024DE11 of library SmBAC1 from
of Schistosoma mansoni, genomic survey sequence
AL621093
AL621093.1 GI:16035235
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                                                                                                                                                                                                 Web: www.genoscope.cns.fr)
Partially Hind III digested and size-selected S. mansoni cercarial DNA was ligated into Hind III digested pBeloBAC 11 vector and used to transform E coli DH10B. The complete library contains 23808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS.
                                                                                                                                                                                                                                                                                  Submitted (05-OCT-2001) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                               Direct Submission
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                                                                                                                                                          from 4 independent sizing-ligation-transformations. Average size ranges from 70-127 kb and genome coverage is 7.9-fold.
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               /db_xref="taxon:6183"
/clone="024DE11"
                                                                           /organism="Schistosoma/mol_type="genomic DNA
                                                                                                                                       Location/Qualifiers
/clone_lib="SmBAC1"
                                                         /strain="Puerto-Rican"
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52.8%;
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Search completed: May 20, 2006, 03:18:35 Job time : 3660 secs
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                                                                                                                         114 ATGATGAT 107
                                                                                 354 CTAATGCTGATGCTGCTGCTGATGATGATGATGCTGCCGCTGCTTATGATGATGATG
                                                             245 GTGGTGGT 252
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Result
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Maximum DB seq length: 2000000000
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /EMC_Celerra_SIDS;

2: /EMC_Celerra_SIDS;

3: /EMC_Celerra_SIDS;

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5: /EMC_Celerra_SIDS;

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7: /EMC_Celerra_SIDS;
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/EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
/EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
/EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
/EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
/EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
/EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
/EMC_Celerra_SIDS3/ptodata/2/ina/PE_COMB.seq:*
/EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
/EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
/EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
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first 45 summaries
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  3 US-09-214-808-1

3 US-09-234-808-1

3 US-09-239-207-13

2 US-08-728-323A-1

3 US-09-40-399-1

3 US-09-410-399-1

3 US-09-410-399-20

3 US-08-770-379-20

3 US-08-770-371A-20

4 US-09-491-356C-7

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1 US-09-181-585-3

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3 US-09-328-352-4107

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Sequence 1, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 3, Appli
Sequence 4107, Appli
Sequence 4107, Appli
Sequence 14, Appli
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44.2	44.4	44.4	44.6	44.6	45	45.2	45.4	45.4	46	46	46.6	46.6	47.6	47.6	47.6	47.8	48.2	48.2	49.2	49.2	49.2
9.7	9.7	9.7	9.7	9.7	9.8	9.9	9.9	9.9	10.0	10.0	10.2	10.2	10.4	10.4	10.4	10.4	10.5	10.5	10.7	10.7	10.7
1129	3334	1740	3210	1518	165	645	195	195	543	533	477	477	615	198	198	2183	234	234	629	198	198
w	w	w	w	w	w	w	ν	N	10	10	w	w	ω	7	7	w	ν	2	ω	7	7
US-10-053-410-1	US-09-668-119-2	US-09-668-119-1	US-09-270-767-13927	US-09-248-796A-5150	US-09-043-303-17	US-09-248-796A-12396	US-08-267-803B-2	US-08-469-802B-2	5273901-6	5482709-5	US-09-684-843A-1	US-09-135-994-1	US-09-248-796A-3155	PCT-US95-10668-4	PCT-US95-10668-3	US-10-104-047-1064	US-08-267-803B-3	US-08-469-802B-3	US-09-533-559-943	PCT-US95-10668-2	PCT-US95-10668-1
Sequence 1, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 13927, A	Sequence 5150, Ap	Sequence 17, Appl	Sequence 12396, A	Sequence 2, Appli	Sequence 2, Appli	Patent No. 5273901	Patent No. 5482709	Sequence 1, Appli	Sequence 1, Appli	Sequence 3155, Ap	Sequence 4, Appli	Sequence 3, Appli	Sequence 1064, Ap	Sequence 3, Appli	Sequence 3, Appli	Sequence 943, App	Sequence 2, Appli	Sequence 1, Appli

## ALIGNMENTS

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	16	16	16	16	- T - NC	TYPE: DNA ORGANISM: 9-214-808	SEQ ID NO	NUMBER OF		CURRENT	EE			APPLICANT:	APPLICANT:	RAL	Sequence 1, Patent No.	1 214-
241	181 16341	121 16281	61 16221	1 16161	Match Local es 28	; TYPE: DNA ; ORGANISM: R US-09-214-808-1	őē. n⊢	S	Tad	FI AP	FER	급 등 -	I do	Ä	Z :	INF	ō ,	RESULT 1 US-09-214-808-1
GAG	AAG	GAC	G-11	ATG	ch 1 Simi 281;	TYPE: DNA ORGANISM: Rhiz 9-214-808-1	ארוא מים	OES	ICAT	FING	FILE REFERENCE:	6475793	NVEN	Pe	T K	ORMA	Appiic 6475793	<u> </u>
TGT	CAG	G — G	0000 0000 00000	ACTO	Match Local Similarity es 281; Conser	TYPE: DNA ORGANISM: Rhizobium 19-214-808-1	л <u>г</u>	ID	NOI	ATIC	,	6475793	INVENTION:	Perret,	Freiberg,	GENERAL INFORMATION	793	•
GTG	AAGC	CATA		JAGA	ity	m	המנמונדוו יפר.	SEQ ID NOS:	MAN	E N	₽₽		g	×	Freiberg,		10.10	
GTTC	CIIGO CAGO	CAGO	ACGT	CTAC	43. ilarity 67. Conservative			1 1	APPLICATION NUMBER:	APPLICATION NUMBER: US/0 FILING DATE: 1999-06-22	CARP0068	D1 a cmid	₩.	2			Application US/09214808A 5475793	ł
TTTC		GCTC	TTCI	TTAC	43.5%; 67.4%; ive			3 (	?	9-06 9-06	i	Э. Э.	mic	면	Andre Christoph		/092	
'AAG'	1001 11011	TCT	AACC	- GG - GG - GG - GG - GG - GG - GG - GG	0			Ċ	ī/ī	JS/0			momic Sequen	1111	ήď		1148	•
CTC	ATCO	3GAA AATG	CACG	AACG 3CGA	Score Pred. Mi				397/	9/21	•		Sequence	ope			ABC	
TCAA	GTAA      GCAA	CATC	TIGI	CTCA GCAA	ore 199.4; ed. No. 5.8 Mismatches				PCT/IB97/00950	US/09/214,808A 16-22			e of					
GCG	61-0 61-0			GEA HE	5.8 Ches				0	A8								
CAC	GTG	0000 	GTT		e 🕒								Rhizobium					
CTTA	CAGG	GCGC	ACIG	CTIG	B 3; 48; 136;													
CTAC	ATGA      ACGA	CGGT	AGCT AGCT	TTG#  -  CAG#	Ler								SP.					
GAGTGTGGTGGTTCTTTCAAGTCTCTCAAGCGTCACCTTACTACTCATCACTCTATGACT	AAGCAGAAGCCTGCTGTTTCTGTTCGTAAGTCTGTTCAGGATGATCATATCGTTTGTTT	GATGTTCATACTGCACTTTCTGGAACATCTGCTCCTGCTTCTGTTGCTGTTAACGTTGAG	GTIGCTGCTTACGTTTCTAACCACGTTGTTCCTGTTACTGAGCTTCCTGGACTTATCTCT	ATGACTGAGACTGCTTACGGTAACGCTCAGGATCTTCTTGTTGAGCTTACTGCTGATATC	Length Indels								NGR					
CAC	TATO	GCT GTT	rgga sacg	PACT	536165								234					
ICTA	GTTT ACCT	AACG — CCCA	CTTA	GCTG  - GCAG									Sym					
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T 300					-								ic					
ŏ	240 16400	180 16340	120 16280	60 16220	0;													

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APPLICANT: Rosenthal, Andre
APPLICANT: Freiberg, Christoph
APPLICANT: Perret, Xavier Philippe
APPLICANT: Broughton, William John
TITLE OF INVENTION: Genomic Sequence of Rhizobium SP.
Patent No. 6475793
TITLE OF INVENTION: Plasmid
FILE REFERENCE: CARPO068
CURRENT APPLICATION NUMBER: US/09/214,808A
CURRENT FILING DATE: 1997-06-22
PRIOR APPLICATION NUMBER: DCT/IB97/00950
PRIOR FILING DATE: 1997-07-10
NUMBER OF SEQ ID NOS: 1
RESULT 3
US-09-639-207-13/c
Gammence 13, Application US/09639207
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US-09-214-808-1/c
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APPLICANT:
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Best Local Similarity
Matches 210; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 536165
TYPE: DNA
ORGANISM: Rhizobium
3-09-214-808-1
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SEQ ID NO 1
                                                                                                                 319721
                                                                                                                                                                                                                                                       319841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 TGTTGAGCTTACTGCTGATATCGTTGCTTGCTTACGTTTCTTAACCACGTTGTTCCTGTTAC 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                        GACCGCAGACTTCATCATATGCCTGGAGGACGGTAAAAAATTCAAATCGCTGAAGCGACA 319842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGATCTGGCCAGTCTTATTCAGCAGACGTATCTCTCGCTATGCAGCACCTCTCAGGCAGA 319962
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                                                                                                                                                                                                                                                                                                                                                                                          CAAGGCTGAGGAGGCTGCCGTCGAAGAACAGCGGCCGCCGTCCCGATCAAGAAGTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                           TGCTTCTGTTGCTGTTAACGTTGAGAAGCCAGAAGCCTGCTGCTTTCTGTTCGTAAGTCTGT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TACGCTGAGGCTCGTTCTCGTCTCGCTAAGGAGATGGGTCTCGGTCAGCGTCGTAAG 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGAGCTTCCTGGACTTATCTCTGATGTTCATACTGCACTTTCTGGAACATCT---GCTCC
                                                                                                               GGGTCTGGGAAAGAAACGGACGGC 319698
                                                                                                                                          GGGTCTCGGTCAGCGTCGTAAGGC 419
                                                                                                                                                                                                                                                     CCTGATGGCTAAGTACGGCCTCACGCCAGCAATATCGAGAGAAATGGGGTCTCCCGGC 319782
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                                                                                                                                                                                  TGATTACCCTATGGTTGCTCCTGCTTACGCTGAGGCTCGTTCTCGTCTCGCTAAGGAGAT 395
                                                                                                                                                                                                                                                                                       CCTTACTACTCATCACTCTATGACTCCAGAGGAGGATATAGAGAGAAGTGGGATCTTCCTGT 335
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Pred. No. 9.4e-17;
0; Mismatches 171; Indels
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RESULT 4

US-08-728-323A-1/c

Sequence 1, Application U
Sequence 1, Spalection U
Patent No. 5948676

GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Russo, Jam
APPLICANT: Russo, Jam
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CURRENT FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: US 60/148,934
PRIOR FILING DATE: 1999-08-12
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: US 60/148,933
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: US 60/177,047
PRIOR PILING DATE: 2000-01-18
PRIOR PILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-05-19
VUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-639-207-13
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APPLICANT: Benzer, Seymour
TITLE OF INVENTION: AN ANIM
TITLE OF INVENTION: TOXICITY
TITLE OF INVENTION: TOXICITY
TITLE OF INVENTION: TOXICITY
FILE REFERENCE: 06618-68600.
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Best Local Similarity
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GENERAL INFORMATION:
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      APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Immediate Early Protein From
TITLE OF INVENTION: Sarcoma-Associated Herpesviru
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48.7%;
בייייייים אומים במדוץ Protein From Kaposi's
Sarcoma-Associated Herpesvirus, DNA
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Pred. No. 2.9e-10;
0; Mismatches 195;
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Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
COMPUTER: PC-DOS/MS-DOS
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
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SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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TELEPHONE: 212-278-0400
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LOCATION:
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STRANDEDNESS: single
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/728,323A
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CTGC 1908
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1185 Avenue of the
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Pred. No. 1.1e-08;
0; Mismatches 225
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GENERAL INFORMATION:

APPLICANT: Kieff, Elliott D.

APPLICANT: Kaleff, Elliott D.

APPLICANT: Kaleff, Elliott D.

APPLICANT: Kaleff, Elliott D.

APPLICANT: Kaye, Kenneth M.

ITILE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE FILE REFERENCE: 16412-10001R

CURRENT APPLICATION NUMBER: US/09/298,568

CURRENT FILING DATE: 1999-04-21

EARLIER APPLICATION NUMBER: US 60/109,422

EARLIER APPLICATION NUMBER: US 60/109,422

EARLIER FILING DATE: 1998-11-19

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 1

LENGTH: 3489
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                                                                                                                                                                                                                         US-09-410-399-1/c
                                                                                                                                                  Sequence 1, Application US/09410399
Patent No. 6482587
GENERAL INFORMATION:
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APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or
TITLE OF INVENTION: to Genomic Host DNA
FILE REFERENCE: UM-03778
CURRENT APPLICATION NUMBER: US/09/410,399
CURRENT FILING DATE: 1999-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Kaposi's sarcoma-associated herpesvirus
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Pred. No. 1.1e-08;
                                                                  Inhibit or Enhance the Binding of Viral Host DNA
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3489
; TYPE: DNA
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-410-399-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
US-09-894-273-1/c
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                                           Query Match
Best Local Simi
Matches 199;
                                                                                                                         LENGTH: 3489
TYPE: DNA
ORGANISM: Kaposi's s
IS-09-894-273-1
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Best Local Similarity 46.9
Matches 199; Conservative
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                                                                                                                                                                                                       SEQ ID NO 1
                                                                                                                                                                                                                   APPLICANT: Kieff, Elliott D.
APPLICANT: Ballestas, Mary E.
APPLICANT: Ballestas, Mary E.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT
TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PER
FILE REFERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US/09/894,273
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/109,422
PRIOR PRIOR APPLICATION NUMBER: US 60/109,422
PRIOR FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
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        CTGAGACTGCTTACGGTAACGCTCAGGATCTTCTTGTTGAGCTTACTGCTGATATCGTTG
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                                               Conservative
                                                                                                                                           sarcoma-associated herpesvirus
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46.9%;
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Pred. No. 1.1e-08;
0; Mismatches 225
                                         Score 64; DB 3;
Pred. No. 1.1e-08;
0; Mismatches 229
                                             225;
                                                                              Length 3489
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US-08-770-379-20
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                         TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 5234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                         ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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             TYPE:
                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
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             nucleic acid
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1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Russo, James J.
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; MOLECULE TYPE:
US-08-770-379-20
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                                    Sequence 20, Application US/08757669A
Patent No. 6183751
GEMERAL INFORMATION:
APPLICANT: Chang, Yuan
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APPLICANT: Bdelman, Isidore S.
APPLICANT: Bdelman, Isidore S.
APPLICANT: MOORE, Patrick S.
APPLICANT: MOORE, PATRICK S.
APPLICANT: MOORE, PATRICK S.
APPLICANT: OF THEREOF
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
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                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 10036
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mes 199; Conserv
                                                                                                                                                                                                                                     CITY: New York
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                                                                                                                                                                                                                                                  B: Cooper & Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                              Bohenzky, Roy A.
Russo, James J.
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                                                                                US/08/757,669A
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                                                                                                             Version
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US-08-757-669A-20
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                                                                                                                                                                                                                                                                                                                                                                                                  US-09-230-371A-20
                                                      SOFTWARE: F
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                APPLICANT: Bdelman, Isidore S
APPLICANT: MOORE, PATTICK S
TITLE OF INVENTION: UNIQUE ASSOCIATED KAP
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 45.85-G-PCT-US
CURRENT APPLICATION NUMBER: US/09/230,371A
CURRENT FILING DATE: 1999-11-17
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                            PRIOR APPLICATION NUMBER: PCT PRIOR FILING DATE: 1997-07-22
                      LENGTH: 32207
TYPE: DNA
ORGANISM: Kaposi's
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TYPE: nucleic acid
STRANDEDNESS: double
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Bohenzky, R
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Pred. No. 2.9e-08;
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                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Philibert, Robert A.
APPLICANT: Ginns, Edward I.
APPLICANT: Gins, Edward I.
APPLICANT: Gins, Edward I.
APPLICANT: Delisi, Lynn
TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
FILE REFERENCE: 9465.6US11
CURRENT APPLICATION NUMBER: US/09/491,356C
CURRENT FILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: PCT/US99/09365
PRIOR APPLICATION NUMBER: FOT/US99/09365
PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1999-04-29
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
SEC 
                                                                                                                                                                               Query Match
Best Local Similarity
Matches 132; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                     LENGTH: 6558
TYPE: DNA
ORGANISM: Mus musculus
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                                                                                                                                                                                                                12.7%;
51.8%;
                                                                                                                                                                                  Score 58.2; DB 3;
Pred. No. 7.6e-07;
0; Mismatches 123;
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                     US-09-491-356C-2/c
US-09-491-356C-2/c
; Sequence 2, Application U
; Patent No. 6566061
; GENERAL INFORMATION:
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  APPLICANT: Philibert,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1748
LENGTH: 6604
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US-09-880-107-1748/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Josep
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1748, Application US/09880107 Patent No. 6974667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Genbank Accession No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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  GAACGG
                                          GIGIGG
                                                                                     TGCTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTCAGGTAGGATGGCTGTT
                                                                                                                              TGCTGCTGCTGCCGGATGTGGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC
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Robert

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RESULT 14
US-09-614-221A-376/c
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                                                                                                                                      ; TYPE: DNA ; ORGANISM: Saccharomyces cerevisiae US-09-614-221A-376
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Best Local Similarity
Matches 128; Conserv
                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/142,981
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 626
SEQ ID NO 376
LENGTH: 2718
                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Karunanandaa, Balasulojini
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 376, Application US/09614221A Patent No. 6723837
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
                                                                     Matches
                                                                                                    Query Match
                                                                                                                                                                                                                                                                           APPLICANT: Yu, Jaehyuk
APPLICANT: Kishore, Ganesh M.
APPLICANT: Kishore, Ganesh M.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
TITLE OF INVENTION: WITH STEROL SYNTHESIS AND METABOLISM
FILE REFERENCE: 16516.075
CURRENT EPPLICATION NUMBER: US/09/614,221A
CURRENT FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/491,356C
CURRENT FILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: PCT/US99/09365
PRIOR FILING DATE: 1999-04-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/083,465 PRIOR FILING DATE: 1998-04-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ginns, Edward I.
APPLICANT: Delisi, Lynn
TITLE OF INVESTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
FILE REFERENCE: 9465.6USI1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 6794
TYPE: DNA
ORGANISM: Homo sapiens
                                                    Local 104;
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                                Similarity
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TGCTGCTGCTGCCGGATGTGGTACTGCTGCTGCTGCTGCTGTTGCTGTTGCTGCTGC 6207
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52.0%;
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Pred. No. 1.5e-06;
0; Mismatches 118;
                                                                   Score 54.2; DB 3;
Pred. No. 7.9e-06;
0; Mismatches 83;
                                                                                                  Length 2718;
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US-09-181-585-3
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CURRENT APPLICATION NUMBER: US/09/181,585

CURRENT FILING DATE: 1998-10-28

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3

LENGTH: 1037
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                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ranum, Laura P.W.
APPLICANT: Koob, Michael
TITLE OF INVENTION: SPINOCEREBELLAR ATAXIA TYPE 8 AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: cDNA OTHER INFORMATION: comprising exons \mathbf{E}, \mathbf{C}, and \mathbf{A}
                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                TTCATACTGCACTTTCTGGAACATCTGCTCCTGCTTCTGTTGCTGTTAACGTTGAGAAGC 184
CTATTTGATGTTATATTGTTATATATTTTTCCATACTTCCTCATACTGCTTATCTC 1000
                                 GTGGTGGTTCTTTCAAGTCTCTCAAGCGTCACCTTACTACTCATCACTCTATGACTC 301
                                                                   CTGCTGCTGCTGCTGCTGCTGCTGCATTTTTAAAAATATATTATCTTATTTTA 943
                                                                                                  AGAAGCCTGCTGTTTCTGTTCGTAAGTCTGTTCAGGATGATCATATCGTTTTGTTTTGGAGT 244
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48.8%;
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Pred. No. 6.8e-06;
0; Mismatches 152;
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Search completed: May 19, 2006, 23:02:42 Job time: 164 secs

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Result
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Maximum
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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291.6
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    No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.

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1: /BMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /BMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*

3: /BMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

4: /BMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US108_PUBCOMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

7: /BMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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US-10-719-996A-1

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US-09-894-273-1

US-10-294-804-1

US-10-194-046-1
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Sequence 5700, Ap	848	Sequence 174145,	Sequence 174387,	Sequence 174235,	Sequence 25433, A	Sequence 631, App	Sequence 2, Appli	Sequence 18999, A	Sequence 75676, A	Sequence 3, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 63, Appl	Sequence 376, App	Sequence 5406, Ap	Sequence 1310, Ap	Sequence 1972, Ap	Sequence 1973, Ap	Sequence 1748, Ap	Sequence 491, App	Sequence 14743, A	Sequence 243, App	Sequence 243, App	Sequence 20174, A	Sequence 325, App	Sequence 166977,

## ALIGNMENTS

System

for Control of Gene

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US-10-719-996A-2

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Publication No. US20040224412A1
GENERAL INFORMATION:
APPLICANT: Hanmoufa, Abdelali
APPLICANT: Hegedua, Dwayne
APPLICANT: Bate, Nicholas
TITLE OF INVENTION: A Repressor-Mediated Regulation
TITLE OF INVENTION: in Plants
FILE REFERENCE: 1096.021A
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Best Local Similarity
Matches 458; Conserv
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CURRENT FILING DATE: 2003-11-21
PRIOR APPLICATION NUMBER: PCT/CA02/00740
PRIOR FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US 60/292,973
PRIOR FILING DATE: 2001-05-23
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TITLE OF INVENTION: A Repressor-Mediated Regulation System for Control of Gene Expres

TITLE OF INVENTION: Plants

FILE REPERENCE: 1096.021B

CURRENT APPLICATION NUMBER: US/10/995,951A

CURRENT FILING DATE: 2004-11-23

PRIOR APPLICATION NUMBER: PCT/CA02/01807

PRIOR FILING DATE: 2002-11-21

PRIOR APPLICATION NUMBER: PCT/CA02/00740

PRIOR APPLICATION NUMBER: PCT/CA02/00740

PRIOR FILING DATE: 2002-05-23

NUMBER OF SEQ ID NOS: 45

SOPTWARE: Patentin version 3.0

SEQ ID NO 2
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Best Local Similarity
Matches 458; Conserv
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TYPE: DNA
ORGANISM: Artificial
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100.0%; Pred. No. 1e-128;
tive 0; Mismatches 0
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APPLICANT: Hegedus, Dwayne
ITITLE OF INVENTION: Repressor Mediated Selection Strategies
FILE REFERENCE: 11089.0003. NEUSO1
CURRENT APPLICATION NUMBER: US/10/678,490
CURRENT FILING DATE: 2003-10-03
PRIOR APPLICATION NUMBER: 60/416,369
PRIOR APPLICATION NUMBER: 60/416,369
PRIOR FILING DATE: 2002-10-03
NUMBER: OF SEQ ID NOS: 61
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 472
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US-10-678-490-1
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APPLICANT: Lydiate, Derek
APPLICANT: Hannoufa, Abdelali
APPLICANT: Bate, Nicholas
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Matches
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Best Local
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ORGANISM: artificial
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Similarity 100.0%;
58; Conservative 0
                                                                                                                                                                                                               GAGTGTGGTGGTTCTTTCAAGTCTCTCAAGCGTCACCTTACTACTCATCACTCTATGACT
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     AACCGTCCAAAAAAGAAGCGTAAGGTCTGAGAGCTCGC 458
                                                                           TACGCTGAGGCTCGTTCTCGTCTCGCTAAGGAGATGGGTCTCGGTCAGCGTCGTAAGGCT
                                                                                                                                                 CCAGAGGAGTATAGAGAGAAGTGGGATCTTCCTGTTGATTACCCTATGGTTGCTCCTGCT
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Pred. No. le-128;
; Mismatches 0;
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434 420 374 360 314 300 254 240 194 180 134 120 74 60

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Sequence 2. Application US/11067425A

Publication No. US20050278809A1

GENERAL INFORMATION:
APPLICANT: Hannoufa, Abdelali
APPLICANT: Hydiate, Derek J.
APPLICANT: Lydiate, Derek J.
APPLICANT: Gao, Ming-Jun

ITILE OF INVENTION. REGULATION OF GENE EXPRESSION USING CHROMATIN REMODELLING FACTORS
FILE REFERENCE: 270.78USI1
CURRENT FAPULCATION NUMBER: US/11/067,425A
CURRENT FAPULCATION NUMBER: US 10/516,753
PRIOR APPLICATION NUMBER: PCT/CA03/00822
PRIOR APPLICATION NUMBER: PCT/CA03/00822
PRIOR APPLICATION NUMBER: US 60/387,088
PRIOR FILING DATE: 2003-06-06
PRIOR FILING DATE: 2002-06-06
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn version 3.3
RESULT 5
US-10-719-996A-3
; Sequence 3, Application US/10719996A
; Publication No. US20040224412A1
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OTHER INFORMATION: Synthetic ROS
US-11-067-425A-2
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LENGTH: 472
TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 458; Conserv
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CURRENT APPLICATION NUMBER: US/10/719,996A
CURRENT FILING DATE: 2003-11-21
PRIOR APPLICATION NUMBER: PCT/CA02/00740
PRIOR FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US 60/292,973
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
SEQ ID NO 3
LENGTH: 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: w is a US-10-719-996A-3
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APPLICANT: Hannoufa, Abdelali
APPLICANT: Hegedua, Dwayne
APPLICANT: Bate, Nicholas
TITLE OF INVENTION: A Repressor-Mediated Regulation
TITLE OF INVENTION: in Plants
FILE REFERENCE: 1096.021A
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Best Local Similarity
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NAME/KEY: misc_feature
1)...(447)
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LOCATION: (1)..(447)
OTHER INFORMATION: y is
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LOCATION: (1)...(447)
OTHER INFORMATION: n is
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OTHER INFORMATION: ROS
FEATURE:
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LOCATION: (1)..(447)
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NAME/KEY: misc_feature
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LOCATION: (1)...(447)
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OTHER INFORMATION: m is
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CCAGAGGAGTATAGAGAGAAGTGGGATCTTCCTGTTGATTACCCTATGGTTGCTTCCTGCT
                                                    GARTGYGGNGGNWSNTTYAARWSNYTNAARMGNCAYYTNACNACNCAYCAYWSNATGACN
                                                                                 GAGTGTGGTGGTTCTTCAAGTCTCTCAAGCGTCACCTTACTACTCATCACTCTATGACT
                                                                                                                    ARCARAARCCNGCNGTNWSNGTNMGNAARWSNGTNCARGAYGAYCAYATHGTNTGYYTN
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58.3%; Pred. No. 9.8e-86;
tive 97; Mismatches 89
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CCNGARGARTAYMGNGARAARTGGGAYYTNCCNGTNGAYTAYCCNATGGTNGCNCCNGCN

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CURRENT APPLICATION NUMBER: US/10/995,951A
CURRENT FILING DATE: 2004-11-23
PRIOR APPLICATION NUMBER: PCT/CA02/01807
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: PCT/CA02/00740
PRIOR FILING DATE: 2002-05-23
VNUMBER OF SEQ ID NOS: 45
SOFTWARE: PATENTIN VETSION 3.0
SEQ ID NO 3
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US-10-995-951A-3
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                                                                                                                                                                                       Query Match
Best Local 9
                                                                                                                                                                       Matches
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TITLE OF INVENTION: A Repressor-Mediated Regulation System for Control of Gene Expre
TITLE OF INVENTION: Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 1096.021B
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TYPE: DNA
ORGANISM: Artificial
                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (1)...(447)
OTHER INFORMATION: w is a or t/u
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LOCATION: (1)..(447)
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NAME/KEY: misc_feature
LOCATION: (1)..(447)
OTHER INFORMATION: n is
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OTHER INFORMATION: ROS consensus sequence
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LOCATION: (1)...(447)
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LOCATION: (1)..(447)
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                                                                                                                                                                                     h 69.2%; Score 317; DB 10;
Similarity 58.3%; Pred. No. 9.8e-86;
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   GATGTTCATACTGCACTTTCTGGAACATCTGCTCCTGCTTCTGTTGCTGTTAACGTTGAG 180
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                                   GTNGCNGCNTAYGTNWSNAAYCAYGTNGTNCCNGTNACNGARYTNCCNGGNYTNATHWSN 120
                                                                  GTTGCTGCTTACGTTTCTAACCACGTTGTTCCTGTTACTGAGCTTCCTGGACTTATCTCT 120
                                                                                                    ATGACNGARACNGCNTAYGGNAAYGCNCARGAYYTNYTNGTNGARYTNACNGCNGAYATH
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PRIOR PILLING DATE: 2004-12-03
PRIOR APPLICATION NUMBER: PCT/CA03/00822
PRIOR FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: US 60/387,088
PRIOR FILING DATE: 2002-06-06
PRIOR FILING DATE: 2002-06-06
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin version 3.3
SEQ ID NO 3
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APPLICANT: Lydiate, Derek J.
APPLICANT: Gao, Ming-Jun
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION USING CHROMATIN REMODELLING
FILE REFERENCE: 270.78USI1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/11/067,425A
CURRENT FILING DATE: 2005-02-22
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NAME/KEY: misc_feature
COATION: (21)...(21)
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LOCATION: (6)...(6)
OTHER_INFORMATION: n is
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OTHER INFORMATION: n is
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LOCATION: (12)..(12)
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SEQ ID NO 19
LENGTH: 429
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Best Local Similarity
                                   Matches 342;
                                               Query Match
Best Local Similarity
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APPLICANT: Hannoufa, Abdelali
APPLICANT: Hannoufa, Abdelali
APPLICANT: Bate, Nicholas
APPLICANT: Hegedus, Dwayne
TITLE OF INVENTION: Repressor Mediated Selection Strategies
FILE REPERENCE: 11089,003.NPUS01
CURRENT APPLICATION NUMBER: US/10/678,490
CURRENT APPLICATION NUMBER: US/10/678,490
CURRENT FILING DATE: 2003-10-03
PRIOR APPLICATION NUMBER: 60/416,369
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 61
NUMBER OF SEQ ID NOS: 61
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; Pred. No. 9.8e-86;
97; Mismatches 89;
                               Score 291.6; DB 8
Pred. No. 5.3e-78;
0; Mismatches 84
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; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-719-996A-1
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US-10-719-996A-1
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
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                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: A Repressor-Mediated Regulation System for Control of Gene Express
TITLE OF INVENTION: in Plants
FILE REFERENCE: 1096.021A
CURRENT APPLICATION NUMBER: US/10/719,996A
CURRENT FILING DATE: 2003-11-21
PRIOR APPLICATION NUMBER: PCT/CA02/00740
PRIOR FILING DATE: 2002-05-23
PRIOR FILING DATE: 2002-05-23
PRIOR FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hannoufa, Abdelali
APPLICANT: Hegedua, Dwayne
APPLICANT: Bate, Nicholas
                                                                                                                                                                                                                Local Similarity nes 342; Conserv
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                                                                                                                                                                                                                 Score 291.6; DB 9
Pred. No. 5.3e-78;
0; Mismatches 84
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; LENGTH: 429
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-995-951A-1
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US-10-995-951A-1
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FILE REFERENCE: 1096.021B
CURRENT APPLICATION NUMBER: US/10/995,951A
CURRENT FILING DATE: 2004-11-23
PRIOR APPLICATION NUMBER: PCT/CA02/01807
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: PCT/CA02/00740
PRIOR APPLICATION NUMBER: PCT/CA02/00740
PRIOR PILING DATE: 2002-05-23
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
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APPLICANT: Hannoufa, A. et al.
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Best Local Similarity
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  TACGCTGAGGCTCGTTCTCGTCTCGCTAAGGATGGGTCTCGGTCAGCGTCGTAAGGCT 420
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Pred. No. 5.3e-78;
0; Mismatches 84;
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US-09-939-964-1
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US-09-939-964-1/c
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Publication No. US20030054522A1
GENERAL INFORMATION:
APPLICANT: Rosenthal, Andre
APPLICANT: Freiberg, Christoph
APPLICANT: Bearret, Xavier Philippe
APPLICANT: Broughton, William John
TITLE OF INVENTION: Genomic Sequence of Rhizobium SP.
TITLE OF INVENTION: Plasmid
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PRIOR FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1
SEQ ID NO 1
Sequence 1, Application US/09939964
Publication No. US20030054532A1
GENERAL INFORMATION:
APPLICANT: Rosenthal, Andre
APPLICANT: Freiberg, Christoph
APPLICANT: Perret, Xavier Philippe
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Best Local
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CURRENT APPLICATION NUMBER: US/09/939,964
CURRENT FILING DATE: 2001-08-27
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TYPE: DNA
ORGANISM: Rhizobium
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Pred. No. 2.6e-48;
Mismatches 136;
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              FILE REFERENCE: 06618-686001
CURRENT APPLICATION NUMBER: US/10/465,217
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: US/09/639,207
PRIOR FILING DATE: 2000-08-14
PRIOR FILING DATE: 2000-08-14
PRIOR FILING DATE: 1999-08-12
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: US 60/148,933
PRIOR FILING DATE: 1999-08-12
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: US 60/177,047
PRIOR FILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 60/205,720
PRIOR APPLICATION NUMBER: US 60/205,720
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-05-19
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US-10-465-217-13/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/10465217
Publication No. US20030204859A1
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Best Local Similarity
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TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
TITLE OF INVENTION: Plasmid
FILE REFERENCE: CARPO068
CURRENT APPLICATION NUMBER: US/09/939,964
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 09/214,808
PRIOR APPLICATION NUMBER: 09/214,808
PRIOR FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                    APPLICANT: Kazemi-Esfarjani, Parsa
APPLICANT: Benzer, Seymour
TITLE OF INVENTION: AN ANIMAL MODEL OF POLYGLUTAMINE
TITLE OF INVENTION: TOXICITY, METHODS OF USE, AND METHOD OF INVENTION: TOXICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Rhizobium
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Pred. No. 2.7e-16;
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CURRENT APPLICATION UNMBER: US/09/894,273
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/109,422
PRIOR FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 3489
TYPE: DNA
ORGANISM: Kaposi's sarcoma-associated herpo
                                                                                                                                                                                                                                                        Sequence 1, Application US/09894273
Publication No. US20040037847A1
GENERAL INFORMATION:
APPLICANT: Kieff, Elliott D.
APPLICANT: Keff, Elliott D.
APPLICANT: Ballestas, Mary E.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: VIRUS DNA TO ME!
FILE REFERENCE: 16412-10001R
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US-09-894-273-1/c
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                                                                                                          US-09-894-273-1
                                                                Query Match
Best Local Similarity
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Best Local Similarity
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SEQ ID NO 13
                                                      Matches
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ORGANISM: Artificial
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CTCTAACTCCTGCTCCTGCTCTAACTCCTGCTCCTGCTCCTGCTGCTGCTCCTGCTC
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                                                                                                                       sarcoma-associated herpesvirus
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                                                   Score 64; DB 3;
Pred. No. 3.8e-08;
0; Mismatches 225
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Pred. No. 8.4e-10;
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                                                                             Length 3489;
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RESULT 15
US-10-294-804-1/c
; Sequence 1, Application US/10294804
; Publication US20030133948A1
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; SEQ ID NO 1
; LENGTH: 3489
; TYPE: DNA
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-10-294-804-1
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Best Local Similarity
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CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: US/09/410,399
PRIOR FILING DATE: 1999-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Robertson, Erle S. APPLICANT: Cotter, Murray A. TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA TITLE OF INVENTION: to Genomic Host DNA FILE REFERENCE: UM-03778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                       199;
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GTGGTGGTTCTTTCAAGTCTCTCAAGCGTCACCTTACTACTCATCACTCTATGACTCCAG 304
                                                                    CTCATCCTGCTGCTCCTCATCCTGCTGCTCCTCATCCTGCTGCTGCTCCTCCTCATC 2092
                                                                                                                                                                                               TTCATACTGCACTTTCTGGAACATCTGCTCCTGCTTCTGTTGCTGTTAACGTTGAGAAGC
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milarity 46.9%;
Conservative

    score 64; DB 7; Length 3489;
    Pred. No. 3.8e-08;
    Mismatches 225; Indels

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Search completed: May 20, 2006, 01:45:40 Job time: 1052 secs

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## November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions .rnpbm (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions .rapbm (Published\_Applications\_AA\_New).

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| EMMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
| EMMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
| MMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
| MMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
| MMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
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US-11-217-529-2664

US-11-217-529-16697

US-11-217-529-175676

US-11-217-529-174145

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US-11-217-529-5700

US-11-217-529-5150

US-11-217-529-562

US-11-217-529-1566

US-11-217-529-173156

US-11-217-529-173156

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Sequence 174187,
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Sequence 5700, Ap
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Sequence 5627, Ap
Sequence 173524,
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Sequence 166977,
Sequence 75676, A
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166819,
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26440, Ap
26444, Ap
3580, Ap
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3580, Ap
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TCTGTTCAGGATGATCATATCGTTTGGTTTTGGAGTGTG	gctcctgcttctgttgctgttaacgttgagaagcagaaacctgctg 	CIGTTACTGAGCTTCCTGGACTTATCTCTGATGTTCATACTGCACTTTCTGGAACATCT 	GATCTTCTTGTTGAGCTTACTGCTGATATCGTTGCTGCTTACGTTTCTAACCACGTTGT	13.1%; Score 60.2; larity 54.8%; Pred. No. 2. Conservative 0; Mismatche	Cation US/11217529 060099612A1 LIMITED YOSHIHISA A, NORIHISA YUKIKO A, TOMOKO A, TOMOKO A, TOMOKO METHODS FOR ANALYZING 8-285 1 UNMBER: US/11/217,529 12004-09-02 12004-09-02 15: 2005-09-02 2004-09-02 15: 197023 Version 3.3	ALIGNMENTS	1809 7 US-11-217-529- 789 7 US-11-217-529- 2787 7 US-11-217-529- 1626 7 US-11-217-529- 1647 7 US-11-217-529- 1767 7 US-11-217-529- 531 7 US-11-217-529- 1833 7 US-11-217-529- 1834 7 US-11-217-529- 1836 7 US-11-217-529- 234 7 US-11-217-529- 3486 7 US-11-217-529- 3487 7 US-11-217-529-
GTGTG 247	GCAGAAGCCTGCTGTTCTGTTCGTAAG 	TGTTCATACTGCACTTTCTGG	TGCTGCTTACGTTTCTAACCA	DB 7; Length 3660; 4e-09; s 98; Indels 0;	GENES OF INDUSTRIAL YE	-	174100 Sequenc 173600 Sequenc 527 Sequenc 173679 Sequenc 18128 Sequenc 1158 Sequenc 16013 Sequenc 173975 Sequenc 76903 Sequenc 76903 Sequenc 17423 Sequenc 250 Sequenc 250 Sequenc 250 Sequenc 250 Sequenc 250 Sequenc 250 Sequenc 250 Sequenc 250 Sequenc 260 Sequenc 27829 Sequenc 27829 Sequenc 279824 Sequenc 279824 Sequenc 279825 Sequenc 279826 Sequenc 279826 Sequenc 279826 Sequenc
	TCGTAAG 210     GCATCTT 854	AACATCT 150    TGTTGCT 914	CGTTGTT 90        TGTTGTT 974	Gaps 0;	YEASTS		e 173600, e 527, App e 173679, A e 1158, Ap e 1158, Ap e 16031, Ap e 16031, Ap e 173975, Ap e 174237, Ap e 174237, Ap e 17529, A e 17529, A

RESULT 2 US-11-217-529-166977/c 밁

853

TCTGCTGTTGAAGATATTGTTCCTGTTGTCGATCTTG

817

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; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75676
                                                                                                                             APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GEI
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
PRIOR FILING DATE: 2004-09-02
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Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAM, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
                                                   NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 75676
LENGTH: 2742
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SEQ ID NO 166977
LENGTH: 936
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ORGANISM: Saccharomyces pastorianus
-11-217-529-166977
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APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: NAKAMURA, YUKIKO
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJINURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
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US-11-217-529-174387/c
, Sequence 174387, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
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Sequence 174235, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
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APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: KUDAMA, YUKIKO
APPLICANT: ASHLKARI, TOSHLHIKO
TITLE OF INVENTION: METHODS FOR APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.3 SEQ ID NO 174235 LENGTH: 231
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Best Local Similarity
Matches 128; Conserv
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PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
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CURRENT FILING DATE: 2005-09-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: S-38-285
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Saccharomyces pastorianus
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                                                                                                                                                TCATACTGCACTTTCTGGAACATCTGCTCCTGCTTCTGTTGCTGTTAACGTTG 178
                                                                                                                                                                                                              TGCTTACGTTTCTAACCACGTTGTTCCTGTTACTGAGCTTCCTGGACTTATCTCTGATGT
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Pred. No. 3.3e-07;
0; Mismatches 125;
                                                                                                                                                                                                                                                                                                             Score 51.4; DB 7; Length 231; Pred. No. 3e-07; o; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANALYZING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENES OF INDUSTRIAL YEASTS
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APPLICANT: SUNTORY LIMITED

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US-11-217-529-174145
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CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTMARE: PatentIn version 3.3
SEQ ID NO 174145
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                                                                                              Query Match
Best Lôcal (
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Best Local Similarity
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TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: -38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
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APPLICANT:
APPLICANT:
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APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
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                                                                                                                                                                                                TYPE: DNA
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                                     25 GCTCAGGATCTTCTTGAGCTTACTGCTGATATCGTTGCTGCTTACGTTTCTAACCAC 84
                                                                                                Similarity
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ASHIKARI, TOSHIHIKO
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NAKAMURA, NORIHISA
KODAMA, YUKIKO
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51.6%;
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                                                                           Score 50.4; DB 7;
Pred. No. 5.4e-07;
0; Mismatches 81;
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Pred. No. 5.7e-07;
0; Mismatches 109;
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CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US/10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
SEQ ID NO 2946
LENGTH: 2151
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US-11-217-529-2946/c
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APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHIE
APPLICANT: KODAMA, YUKIKO
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SOFTWARE: Patentin version 3
SEQ ID NO 5700
LENGTH: 2142
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APPLICANT: SUNTORY LIMITED
                                                                                                                                                                                                                                                                                                                                                                      Sequence 2946, Application US/11217529
Publication No. US20060099612A1
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                                                                                                                                                                                   APPLICANT: NAKAMURA, NORIHISA APPLICANT: KODAMA, YUKIKO APPLICANT: FUJIMURA, TOMOKO APPLICANT: ASHIKARI, TOSHIHIKO TITLE OF INVENTION: METHODS FOR FILE REFERENCE: S-38-285
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CURRENT FILING DATE: 2005-09-02
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APPLICANT: ASHLKARI, TOSHLHIKO
APPLICANT: ASHLKARI, TOSHLHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
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APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
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TYPE: DNA
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Pred. No. 1.8e-06;
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                                                                                                                                                                                                             GENES OF INDUSTRIAL YEASTS
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US-11-217-529-5627/c
; Sequence 5627, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
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US-11-217-529-2150/c
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Best Local Similarity
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LENGTH: 2304
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Publication No. US20060099612A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Saccharomyces pastorianus
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                                                                                                                                                                                                                                                               TGCACTTTCTGGAACATCTGCTCCTGCTTCTGTTGCTGTTAACGTTGAGAAGCAGAAGCC 191
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Pred. No. 1.3e-05;
0; Mismatches 109; Indels
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Pred. No. 3.7e-06;
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CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER: OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 5627
LENGTH: 1239
TYPE: DATE
ORGANISM: Saccharomyces pastorianus
US-11-217-529-5627
                                                                                                                                                                                                           FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOPTWARE: Patentin version 3.3
SEQ ID NO 173524
LENGTH: 159
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
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Enablication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHHIRO
APPLICANT: NAKAO, YOSHHIRO
APPLICANT: NAKAO, YUKIKO
APPLICANT: KODAMA, YUKIKO
                                                                                                                                       Query Match
Best Local :
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APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR
FILE REFERENCE: S-38-285
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: FUJIMURA, TOMOKO APPLICANT: ASHIKARI, TOSHIHIKO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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  121 GATGTTCATACTGCACTTTCTGGAACATCTGCTCCTGCTTCTGTTGCTGTTAACGTTGAG 180
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                                                                                                                                       Similarity
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                                       GTTGCTGCTTACGTTTCTAACCACGTTGTTCCTGTTACTGAGCTTCCTGGACTTATCTCT
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KODAMA, YUKIKO
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                                                                                                                   Score 46.2; DB 7;
Pred. No. 9.6e-06;
0; Mismatches 63;
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RESULT 13
US-11-217-529-856/c
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US-11-217-529-173156/c
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APPLICANT: NAKAN, YOSHIHISA
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YURIKO
APPLICANT: KODAMA, YURIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GEI
FILE REFERENCE: S-38-285
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                     APPLICANT: NAKAMÜRA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                             APPLICANT: SUNTORY LIMITED APPLICANT: NAKAO, YOSHIHIRO
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ORGANISM: Saccharomyces pastorianus
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Pred. No. 3.1e-05;
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                                                                                                                                                        OF INDUSTRIAL YEASTS
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Best Local Similarity
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Best Local Similarity 51.8%;
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                                                                                                                                                                                                                                                                                                                                                                                           Matches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SUNTORY LIMITED APPLICANT: NAKAO, YOSHIHIRO APPLICANT: NAKAMURA, NORIHISA APPLICANT: KODAMA, YUKIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 6948
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1728 AGTGCTGTTTTGTTGCG 1712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1908 ACCÓCCACCACTGCTGCTGATGATGATGTTGTTGCTATTGCTGTTGCCGTTGCTGTT 1849
                                                                                                                                                                                                                       923
                                                 803 GCATTAGCGGTGTTGTTGTTATTGTTGTTTGTTACTGGAC 762
                                                                                                                                                                            162
                                                                                                                                                                                                                                                             102 GCTTCCTGGACTTATCTCTGATGTTCATACTGCACTTTCTGGAACATCTGCTCCTGCTTC 161
                                                                                                                                                                                                                                                                                                        10 ACTGCTTACGGTAACGCTCAGGATCTTCTTGTTGAGCTTACTGCTGATATCGTTGCTGCT
                                                                                                                                                                                                                                                                                                                                                42 TGAGCTTACTGCTGATATCGTTGCTGCTTACGTTTCTAACCACGTTGTTCCTGTTACTGA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 TACGTTTCTAACCACGTTGTTCCTGTTACTGAGCTTCCTGGACTTATCTCTGATGTTCAT
                                                                                                                                                                                                                       TGTTGCTGTTGTTGCTGCATTTTCAATTGTTGCAAATGTTGCATTTGTTGTAACGAT 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ccrecrerrected
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                                                                                     TGATCATATCGTTTGTTTGGAGTGTGGTGGTTCTTTCAAGTC
                                                                                                                                  TGTTGCATATTTTGCTGAGTAGCAATATTGTTCGCATTATTGTTATTGCCGGTAACAGGA
                                                                                                                                                                            TGTTGCTGTTAACGTTGAGAAGCAGAAGCCTGCTGTTTCTGTTCGTAAGTCTGTTCAGGA
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                             9.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                               Score 42.8; DB 7;
Pred. No. 0.00026;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.00014;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 6948;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 990;
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RESULT 15
US-11-217-529-174534/c
Sequence 174534, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: KODAMA, YUKINO
APPLICANT: KODAMA, YUKINO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITIE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
SEQ ID NO 174534
LENGTH: 1368
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-174534
Search completed: May 20, 2006, 01:28:01 Job time : 20 secs
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                                                                                                                                                                                                                                                                                                                                                              406 GT 405
                                                                                                                                   232 GT 233
                                                                                                                                                                                   466 GTAATTGCAGCTGTTGCTGCATCTGCTGCTGGTGAGTCAATTGAGGTTGCAGATTGG 407
                                                                                                                                                                                                                    172 AACGTTGAGAAGCAGAAGCCTGCTGTTTCTGTTCGTAAGTCTGTTCAGGATGATCATATC 231
                                                                                                                                                                                                                                                                         112 CTTATCTCTGATGTTCATACTGCACTTTCTGGAACATCTGCTCCTGCTTCTGTTGCTGTT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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